



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 191168

TO: Juliet Switzer
Location: rem/2A61/2C70
Art Unit: 1634
Friday, June 09, 2006
Case Serial Number: 09/865579

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Switzer,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian (ASRC Aerospace)
STIC Biotech/Chem Library
(571)272-4161

*orange
sheet*

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 62.5679 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-18
Perfect score: 28
Sequence: 1 aaattgggtacaaagtatacttcgtt 28

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTUS_COMB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq.*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq.*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
2	28	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
3	28	100.0	2028	3	US-09-134-001C-1710 Sequence 1710, App
C 4	18.6	66.4	601	3	US-09-949-016-43987 Sequence 43987, A
C 5	18.6	66.4	55387	3	US-09-949-016-43987 Sequence 12993, A
C 6	18.4	65.7	37030	3	US-08-311-731A-25 Sequence 25, Appl
C 7	18	64.3	232	4	US-09-880-107-262 Sequence 262, App
C 8	17.8	63.6	465	3	US-09-270-767-6011 Sequence 6011, App
C 9	17.8	63.6	465	3	US-09-270-767-21293 Sequence 21293, A
C 10	17.6	62.9	452	3	US-08-956-171E-582 Sequence 582, App
C 11	17.6	62.9	452	3	US-08-781-986A-582 Sequence 582, App
C 12	17.6	62.9	601	3	US-09-949-016-198083 Sequence 198083, A
C 13	17.6	62.9	601	3	US-09-949-016-198084 Sequence 198084, A
C 14	17.6	62.9	792	3	US-09-583-110-2286 Sequence 2286, App
C 15	17.6	62.9	792	3	US-09-107-433-1010 Sequence 1010, App
C 16	17.6	62.9	4371	3	US-09-134-000C-3022 Sequence 3022, App
C 17	17.6	62.9	7263	3	US-09-562-702A-31 Sequence 31, Appl
C 18	17.6	62.9	7263	3	US-09-561-818A-27 Sequence 27, Appl
C 19	17.6	62.9	7263	3	US-10-037-182-19 Sequence 19, Appl
C 20	17.6	62.9	7554	3	US-09-562-702A-29 Sequence 29, Appl
C 21	17.6	62.9	7554	3	US-09-561-818A-25 Sequence 25, Appl
C 22	17.6	62.9	7554	3	US-10-037-182-17 Sequence 17, Appl
C 23	17.6	62.9	24020	3	US-09-949-016-17353 Sequence 17353, A

C 24 17.6 62.9 96074 3 US-09-949-016-12760 Sequence 12760, A
C 25 17.6 62.9 96074 3 US-09-949-016-13611 Sequence 13611, A
C 26 17.6 62.9 110000 3 US-09-830-902-1 Sequence 1, Appli
C 27 17.6 62.9 4403765 3 US-09-103-840A-2 Sequence 2, Appli
C 28 17.6 62.9 4411529 3 US-09-103-840A-1 Sequence 1, Appli
C 29 17.4 62.1 1233 5 US-09-974-300-2472 Sequence 2472, Ap
C 30 17.4 62.1 1318 3 US-09-183-253-3 Sequence 3, Appli
C 31 17.4 62.1 1983 3 US-09-452-638-50 Sequence 50, Appl
C 32 17.4 62.1 1983 3 US-09-121-587A-1 Sequence 1, Appli
C 33 17.4 62.1 3175 3 US-09-799-451-793 Sequence 793, App
C 34 17.4 62.1 4249 3 US-09-071-035-403 Sequence 403, App
C 35 17.4 62.1 4249 3 US-10-206-576-403 Sequence 403, App
C 36 17.4 62.1 4359 3 US-09-071-035-401 Sequence 401, App
C 37 17.4 62.1 4359 3 US-10-206-576-401 Sequence 401, App
C 38 17.4 62.1 84495 3 US-09-797-906-3 Sequence 3, Appli
C 39 17 60.7 220 3 US-09-513-999C-14621 Sequence 14621, A
C 40 17 60.7 293 3 US-09-854-133-534 Sequence 534, App
C 41 17 60.7 601 3 US-09-949-016-124786 Sequence 124786,
C 42 17 60.7 601 3 US-09-949-016-144670 Sequence 144670,
C 43 17 60.7 601 3 US-09-949-016-144671 Sequence 144671,
C 44 17 60.7 1583 4 US-10-094-743-1469 Sequence 1469, Ap
C 45 17 60.7 1761 3 US-09-248-796A-6869 Sequence 6869, Ap

ALIGNMENTS

RESULT 1

US-08-743-637B-169
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 2007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 2
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match
Best Local Similarity 100.0%; Score 28; DB 3; Length 2007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 3
US-09-134-001C-1710
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
```

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match
Best Local Similarity 100.0%; Score 28; DB 3; Length 2028;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28
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Db 630 AAATTGGGTACAAGATGATACCTTCGTT 657

RESULT 4
US-09-949-016-43987/c
; Sequence 43987, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43987
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-43987

Query Match
Best Local Similarity 66.4%; Score 18.6; DB 3; Length 601;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 254 TTGGGTACAAGATGATACCTTCGTT 230

RESULT 5
US-09-949-016-12993/c
; Sequence 12993, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12993
LENGTH: 55387
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(55387)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12993

Query Match 66.4%; Score 18.6; DB 3; Length 55387;
Best Local Similarity 84.0%; Pred. No. 1e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TTGGGTACAGATGATACCTTCGTT 28
||||| ||| ||||| |||
Db 20965 TTGGGTACAGAGATGATACCTTCGTT 20941

RESULT 6
US-08-311-731A-25/c
Sequence 25, Application US/08311731A
Patent No. 6583266
GENERAL INFORMATION:
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSER: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 37030 base pairs
TYPE: nucleic acid
STRADEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
ORGANISM: MYCOBACTERIUM LEPRAE
US-08-311-731A-25

Query Match 65.7%; Score 18.4; DB 3; Length 37030;
Best Local Similarity 78.6%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
||||| ||| ||||| ||||| |||||
Db 8487 AAATTCGTCAGATGATACCTTCGAT 8460

RESULT 7
US-09-880-107-262
Sequence 262, Application US/09880107
Patent No. 6974667
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 262
LENGTH: 232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. 6974667 AAL29390
US-09-880-107-262

Query Match 64.3%; Score 18; DB 4; Length 232;
Best Local Similarity 80.8%; Pred. No. 87;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATTGGGTACAGATGATACCTTCGTT 28
||||| ||| ||||| ||||| |||||
Db 172 ATTGGTACATGATGATACCTTCGTT 197

RESULT 8
US-09-270-767-6011/c
Sequence 6011, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6011
LENGTH: 465
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-6011

Query Match 63.6%; Score 17.8; DB 3; Length 465;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ATTGGGTACAGATGATACCT 23
||||| ||| ||||| ||||| |||||

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Db      201 ATTGGGTACAGGATACCT 181
RESULT 9
US-09-270-767-21293/c
; Sequence 21293, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21293
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-21293
Query Match      63.6%; Score 17.8; DB 3; Length 465;
Best Local Similarity 90.5%; Pred. No. 1.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3 ATTGGGTACAGGATACCT 23
Db      201 ATTGGGTACAGGATACCT 181
RESULT 10
US-08-956-171E-582
; Sequence 582, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353
RESULT 11
US-08-781-986A-582
; Sequence 582, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353
RESULT 12
US-09-949-016-198083/c
; Sequence 198083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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;
; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 582:
US-08-956-171E-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353
RESULT 11
US-08-781-986A-582
; Sequence 582, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 582:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-582
Query Match      62.9%; Score 17.6; DB 3; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAAGATGATACCTTC 25
Db      330 AATTGGTAAACAAGATAATACCTAC 353
RESULT 12
US-09-949-016-198083/c
; Sequence 198083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 198083
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-198083

Query Match 62.9%; Score 17.6; DB 3; Length 601;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTT 24
 Db 110 AGAGTGGGTACAAGGTGATACCAT 87

RESULT 13
 US-09-949-016-198084/c
 ; Sequence 198084, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 198084
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-198084

Query Match 62.9%; Score 17.6; DB 3; Length 601;
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTT 24
 Db 532 AGAGTGGGTACAAGGTGATACCAT 509

RESULT 14
 US-09-583-110-2286/c
 ; Sequence 2286, Application US/09583110
 ; Patent No. 6699703
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al.
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
 ; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
 ; FILE REFERENCE: PATH00-07A
 ; CURRENT APPLICATION NUMBER: US/09/583,110
 ; CURRENT FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433
 ; PRIOR FILING DATE: 1998-06-30
 ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; PRIOR FILING DATE: 1998-05-12
 ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; PRIOR FILING DATE: 1997-07-02
 ; NUMBER OF SEQ ID NOS: 5322
 ; SEQ ID NO 2286
 ; LENGTH: 792
 ; TYPE: DNA
 ; ORGANISM: Streptococcus pneumoniae
 US-09-583-110-2286

Query Match 62.9%; Score 17.6; DB 3; Length 792;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AATTGGGTACAAGATGATACCTT 25
 Db 408 AACTGGGTACAAGCTGATACCTT 385

RESULT 15
 US-09-107-433-1010/c
 ; Sequence 1010, Application US/09107433
 ; Patent No. 6800744
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
 ; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
 ; THERAPEUTICS
 ; NUMBER OF SEQUENCES: 5206
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 ; STREET: 100 Beaver Street
 ; CITY: Waltham
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02354
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: CD-ROM ISO9660
 ; COMPUTER: <Unknown>
 ; OPERATING SYSTEM: <Unknown>
 ; SOFTWARE: <Unknown>
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/107,433
 ; FILING DATE: 30-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/ 085131
 ; FILING DATE: May 12, 1998
 ; APPLICATION NUMBER: 60/051553
 ; FILING DATE: July 2, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ariniello, Pamela Deneke
 ; REGISTRATION NUMBER: 40,489
 ; REFERENCE/DOCKET NUMBER: GTC-011
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (781)893-5007
 ; TELEFAX: (781)893-8277
 ; INFORMATION FOR SEQ ID NO: 1010:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 792 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Streptococcus pneumoniae
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (B) LOCATION 1...792

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; SEQUENCE DESCRIPTION: SEQ ID NO: 1010:
US-09-107-433-1010
  Query Match      62.9%; Score 17.6; DB 3; Length 792;
  Best Local Similarity 83.3%; Pred. No. 1.6e+02;
  Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AATTGGGTACAGATGATACCTTC 25
Db      408 AACTTGGTACAGCTGATAACTTC 385

Search completed: May 31, 2006, 21:13:00
Job time : 66.5679 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: May 31, 2006, 21:16:53 ; Search time 727.424 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-18
Perfect score: 28
Sequence: 1 aaattgggtacaaatgatacttcgtt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:
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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:
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15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	28	3	US-09-865-579A-18
2	28	100.0	560	10	US-10-478-633A-150
3	28	100.0	1957	9	US-10-479-674-82
4	28	100.0	2007	3	US-09-452-599-169
5	28	100.0	2007	7	US-10-121-120-169
6	28	100.0	2007	9	US-10-479-674-78
7	28	100.0	2007	9	US-10-479-674-90
8	28	100.0	2007	9	US-10-121-120-169
9	28	100.0	2028	8	US-10-724-972A-3141
10	26.4	94.3	2007	9	US-10-479-674-91
11	20.6	73.6	1400	16	US-11-128-061-4115
12	20.6	73.6	1400	16	US-11-128-049-4115
13	20.6	73.6	2858	16	US-11-128-061-473
14	20.6	73.6	2858	16	US-11-128-049-473
15	20	71.4	20	10	US-10-478-633A-153
16	20	71.4	3800	8	US-10-398-221-3698
17	19.6	70.0	306	9	US-10-425-115-140327

C 18	19.6	70.0	2910	9	US-10-425-115-126781	Sequence 126781,
C 19	19.6	70.0	2331	9	US-10-425-115-126780	Sequence 126780,
C 20	19.2	68.6	595	12	US-10-301-480-472753	Sequence 472753,
C 21	19.2	68.6	595	12	US-10-301-480-1086162	Sequence 1086162,
C 22	19.2	68.6	605	4	US-09-925-065A-406025	Sequence 406025,
C 23	19.2	68.6	605	5	US-09-925-065A-406025	Sequence 406025,
C 24	19	67.9	576	8	US-10-282-122A-10503	Sequence 10503, A
C 25	19	67.9	591	8	US-10-282-122A-9815	Sequence 9815, Ap
C 26	19	67.9	856	12	US-10-301-480-561542	Sequence 561542,
C 27	19	67.9	856	12	US-10-301-480-1174951	Sequence 1174951,
C 28	19	67.9	879	6	US-10-027-632-8631	Sequence 8631, Ap
C 29	19	67.9	879	7	US-10-027-632-8631	Sequence 8631, Ap
C 30	18.6	66.4	529	7	US-10-029-386-7679	Sequence 7679, Ap
C 31	18.4	65.7	362	4	US-09-925-065A-109347	Sequence 109347,
C 32	18.4	65.7	362	5	US-09-925-065A-109347	Sequence 109347,
C 33	18.4	65.7	381	10	US-10-779-543-11069	Sequence 11069, A
C 34	18.4	65.7	381	12	US-10-301-480-465371	Sequence 465371,
C 35	18.4	65.7	381	12	US-10-301-480-1078780	Sequence 1078780,
C 36	18.4	65.7	384	4	US-09-925-065A-397844	Sequence 397844,
C 37	18.4	65.7	384	5	US-09-925-065A-397844	Sequence 397844,
C 38	18.4	65.7	395	12	US-10-301-480-210272	Sequence 210272,
C 39	18.4	65.7	395	12	US-10-301-480-823681	Sequence 823681,
C 40	18.4	65.7	396	4	US-09-925-065A-110802	Sequence 110802,
C 41	18.4	65.7	396	5	US-09-925-065A-110802	Sequence 110802,
C 42	18.4	65.7	450	4	US-09-925-065A-573590	Sequence 573590,
C 43	18.4	65.7	450	4	US-09-925-065A-573591	Sequence 573591,
C 44	18.4	65.7	450	4	US-09-925-065A-573593	Sequence 573593,
C 45	18.4	65.7	450	5	US-09-925-065A-573590	Sequence 573590,

ALIGNMENTS

RESULT 1

US-09-865-579A-18
; Sequence 18, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Saio, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; CURRENT APPLICATION NUMBER: JP 2000-163149
; FILE REFERENCE: 9558-003-27
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-18

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAATGATACCTTCGTT 28

Db 1 AAATTGGGTACAAATGATACCTTCGTT 28

RESULT 2

US-10-478-633A-150
; Sequence 150, Application US/10478633A
; Publication No. US20050059000A1

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; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 150
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-150

Query Match      100.0%; Score 28; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 368 AAATTGGGTACAGATGATACCTTCGTT 395

RESULT 3
US-10-479-674-82
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTAN
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 28; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 559 AAATTGGGTACAGATGATACCTTCGTT 586

RESULT 4
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
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; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 608 AAATTGGGTACAGATGATACCTTCGTT 635

RESULT 5
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAGATGATACCTTCGTT 28
Db 608 AAATTGGGTACAGATGATACCTTCGTT 635

RESULT 6
US-10-479-674-78
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; CURRENT FILING DATE: 1999-12-01
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; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 78

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-78

Query Match 100.0%; Score 28; DB 9; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 7

US-10-479-674-90

; Sequence 90, Application US/10479674

; Publication No. US20050019893A1

; GENERAL INFORMATION:

; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Rosebach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT

; FILE REFERENCE: TV/12287.92

; CURRENT APPLICATION NUMBER: US/10/479,674

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 90

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-90

Query Match 100.0%; Score 28; DB 9; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 609 AAATTGGGTACAAGATGATACCTTCGTT 636

RESULT 8

US-10-121-120-169

; Sequence 169, Application US/10121120

; Publication No. US20050042606A9

; GENERAL INFORMATION:

; APPLICANT: Bergeron, Michel G.

; APPLICANT: Ouellette, Marc

; APPLICANT: Roy, Paul H.

; TITLE OF INVENTION: Specific and Universal Probes and Amplification

; TITLE OF INVENTION: Primers

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical

; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

; FILE REFERENCE: 12287.31

; CURRENT APPLICATION NUMBER: US/10/121,120

; CURRENT FILING DATE: 2002-04-11

; PRIOR APPLICATION NUMBER: 09/452,599

; PRIOR FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: 08/304,732

; PRIOR FILING DATE: 1994-09-12

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 169

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

Query Match 94.3%; Score 26.4; DB 9; Length 2007;

Best Local Similarity 96.4%; Pred. No. 0.11;

Matches 27; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

US-10-121-120-169

Query Match 100.0%; Score 28; DB 9; Length 2007;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 608 AAATTGGGTACAAGATGATACCTTCGTT 635

RESULT 9

US-10-724-972A-3141

; Sequence 3141, Application US/10724972A

; Publication No. US20040147734A1

; GENERAL INFORMATION:

; APPLICANT: Doucette-Stamm, Lynn

; APPLICANT: Bush, David

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: PATH03-16

; CURRENT APPLICATION NUMBER: US/10/724,972A

; CURRENT FILING DATE: 2003-12-01

; PRIOR APPLICATION NUMBER: 09/450,969

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: 09/134,001

; PRIOR FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 7544

; SEQ ID NO 3141

; LENGTH: 2028

; TYPE: DNA

; ORGANISM: S.epidermidis

US-10-724-972A-3141

Query Match 100.0%; Score 28; DB 8; Length 2028;

Best Local Similarity 100.0%; Pred. No. 0.02;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTTCGTT 28

|||||

Db 630 AAATTGGGTACAAGATGATACCTTCGTT 657

RESULT 10

US-10-479-674-91

; Sequence 91, Application US/10479674

; Publication No. US20050019893A1

; GENERAL INFORMATION:

; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Rossbach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT

; FILE REFERENCE: TV/12287.92

; CURRENT APPLICATION NUMBER: US/10/479,674

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 91

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-91

Qy 1 AATTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 609 AAATGGGTACAAGATGATACCTTCGTT 636

RESULT 11
US-11-128-061-4115/c
; Sequence 4115, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4115
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Cricetinae gen. sp.
US-11-128-061-4115

Query Match 73.6%; Score 20.6; DB 16; Length 1400;
Best Local Similarity 85.2%; Pred. No. 54;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AATTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 566 AATTGGGTACAATCTGAGACCTTCATT 540

RESULT 12
US-11-128-049-4115/c
; Sequence 4115, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4115
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Cricetinae gen. sp.
US-11-128-049-4115

Query Match 73.6%; Score 20.6; DB 16; Length 1400;
Best Local Similarity 85.2%; Pred. No. 54;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AATTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 566 AATTGGGTACAATCTGAGACCTTCATT 540

RESULT 13
US-11-128-061-473/c
; Sequence 473, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 473
; LENGTH: 2858
; TYPE: DNA
; ORGANISM: Cricetinae gen. sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (129)..(191)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (366)..(400)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (405)..(423)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (481)..(501)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1020)..(1034)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-473

Query Match 73.6%; Score 20.6; DB 16; Length 2858;
Best Local Similarity 85.2%; Pred. No. 64;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AATTGGGTACAAGATGATACCTTCGTT 28
|||||
Db 2024 AATTGGGTACAATCTGAGACCTTCATT 1998

RESULT 14
US-11-128-049-473/c
; Sequence 473, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.

APPLICANT: Leonard, Mark W.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
TITLE OF INVENTION: MAKING AND USING SAME
FILE REFERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT FILING DATE: 2005-05-11
PRIOR APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: PatentIn version 3.3
SEQ ID NO 473
LENGTH: 2858
TYPE: DNA
ORGANISM: Cricetinae gen. sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (129)..(191)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (366)..(400)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (405)..(423)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (481)..(501)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc feature
LOCATION: (1020)..(1034)
OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-473

Query Match 73.6%; Score 20.6; DB 16; Length 2858;
Best Local Similarity 85.2%; Pred.No. 64;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AATTGGGTACAGATGATACCTTCGTT 28
|||||
DB 2024 AATTGGGTACAGATGATACCTTCATT 1998

RESULT 15
US-10-478-633A-153/c
Sequence 153, Application US/10478633A
Publication No. US20050059000A1
GENERAL INFORMATION:
APPLICANT: TAKARA BIO INC.
TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
TITLE OF INVENTION: acid amplification or detection reaction
FILE REFERENCE: 663232
CURRENT APPLICATION NUMBER: US/10/478,633A
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: JP 2001-177737
PRIOR FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: JP 2001-249689
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 153
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Designed chimeric oligonucleotide primer designated as Meca-A611
OTHER INFORMATION: amplify a portion of Meca gene from Staphylococcus aureus. "Nucle
OTHER INFORMATION: are ribonucleotides-other nucleotides are deoxyribonucleotides."
US-10-478-633A-153

Query Match 71.4%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTGGGTACAAAGATGATACCT 23
|||||
DB 20 TTGGGTACAAAGATGATACCT 1

Search completed: May 31, 2006, 23:02:16
Job time : 728.424 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 10.716 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-18
Perfect score: 28
Sequence: 1 aaattgggtacaaatgatacttcggtt 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.6	62.9	1397	6	US-10-953-349-20718, A
2	17	60.7	2367	7	US-11-121-154-185, A
3	16.8	60.0	966	7	US-11-217-529-174552, A
4	16.8	60.0	1476	7	US-11-217-529-304, A
5	16.8	60.0	3561	7	US-11-121-154-58, A
6	16.8	60.0	16351	6	US-10-501-834-217, A
7	16.4	58.6	660	6	US-10-953-349-6113, A
8	16.4	58.6	1852	6	US-10-953-349-14597, A
9	16.2	57.9	25	7	US-11-217-529-105721, A
10	16.2	57.9	351	7	US-11-217-529-77397, A
11	16.2	57.9	3054	6	US-10-505-928-492, A
12	16	57.1	378	7	US-11-217-529-82662, A
13	16	57.1	1501	6	US-10-953-349-3885, A
14	16	57.1	1811	6	US-10-953-349-28833, A
15	16	57.1	1821	6	US-10-953-349-5704, A
16	15.8	56.4	606	7	US-11-249-111-27, A
17	15.8	56.4	756	7	US-11-217-529-82078, A
18	15.8	56.4	1200	7	US-11-217-529-79719, A
19	15.8	56.4	1309	6	US-10-953-349-7709, A
20	15.8	56.4	1347	7	US-11-217-529-76835, A
21	15.8	56.4	2896	7	US-11-293-697-281, A
22	15.8	56.4	3165	7	US-11-217-529-75763, A
23	15.6	55.7	521	6	US-10-488-619-2432, A
24	15.6	55.7	728	6	US-10-953-349-37612, A
25	15.6	55.7	1566	6	US-10-953-349-83326, A

ALIGNMENTS

RESULT 1

US-10-953-349-20718
; Sequence 20718, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20718
; LENGTH: 1397
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20718

Query Match 62.9%; Score 17.6; DB 6; Length 1397;
Best Local Similarity 83.3%; Pred. No. 8.7;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAGATGATACCTT 24
Db 300 AAAATGGGTACAGAGGATACCTT 323

RESULT 2

US-11-121-154-185
; Sequence 185, Application US/11121154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, LARRY EDMUND
; APPLICANT: WEINER, RONALD M.
; APPLICANT: HUTCHESON, STEVEN WAYNE
; APPLICANT: ERBORG, NATHAN A.
; APPLICANT: HOWARD, MICHAEL
; TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
; FILE REFERENCE: 108172-00121
; CURRENT APPLICATION NUMBER: US/11/121,154
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,971
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185
; LENGTH: 2367

; TYPE: DNA
; ORGANISM: Microbulbifer degradans
US-11-121-154-185

Query Match 60.7%; Score 17; DB 7; Length 2367;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 TTGGTACAAGATGATACCTTCGTT 28
Db 1584 TTGGTACAAGATGGCTCTTCGTT 1608

RESULT 3
US-11-217-529-174552
; Sequence 174552, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174552
; LENGTH: 966
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174552

Query Match 60.0%; Score 16.8; DB 7; Length 966;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
Db 242 AAAAGGGTACAACGCTGATACATCCGAT 269

RESULT 4
US-11-217-529-304
; Sequence 304, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 304
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-304

Query Match 60.0%; Score 16.8; DB 7; Length 1476;

Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TACAAGATGATACCTTCGTT 28
Db 161 TACAAGATGGTACCTTCGTT 180

RESULT 5
US-11-121-154-58
; Sequence 58, Application US/11121154
; Publication No. US20060105914A1
; GENERAL INFORMATION:
; APPLICANT: TAYLOR, LARRY EDMUND
; APPLICANT: WEINER, RONALD M.
; APPLICANT: HUTCHESON, STEVEN WAYNE
; APPLICANT: EKBOG, NATHAN A.
; APPLICANT: HOWARD, MICHAEL
; TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
; FILE REFERENCE: 108172-00121
; CURRENT APPLICATION NUMBER: US/11/121,154
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,971
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 3561
; TYPE: DNA
; ORGANISM: Microbulbifer degradans
US-11-121-154-58

Query Match 60.0%; Score 16.8; DB 7; Length 3561;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
Db 1101 AGATTGGGTAAAAGTTGCTACGTCGAT 1128

RESULT 6
US-10-501-834-217/c
; Sequence 217, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; TITLE OF INVENTION: and Proteins
; FILE REFERENCE: 07039/386US1
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 16351
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-501-834-217

Query Match 60.0%; Score 16.8; DB 6; Length 16351;
Best Local Similarity 75.0%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AAATTGGGTACAAGATGATACCTTCGTT 28
Db 8069 AATTGGTTATAGGTTTATACCTTCATT 8042

```
RESULT 7
US-10-953-349-6113
; Sequence 6113, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6113
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6113

Query Match      58.6%; Score 16.4; DB 6; Length 660;
Best Local Similarity 76.9%; Pred. No. 28;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 ATTGGGTACAAGATGATACCTTCGTT 28
DB 454 AATTGGTACTTGACGATACCTTCITT 479

RESULT 8
US-10-953-349-14597
; Sequence 14597, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14597
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-14597

Query Match      58.6%; Score 16.4; DB 6; Length 1852;
Best Local Similarity 76.9%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 ATTGGGTACAAGATGATACCTTCGTT 28
DB 1657 ATTATCTAAAGATGATACCTTCGTT 1682

RESULT 9
US-11-217-529-105721/c
; Sequence 105721, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
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; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105721
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-105721

Query Match      57.9%; Score 16.2; DB 7; Length 25;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATTGGGTACAAGATGATACC 22
DB 25 AATTGGGTATAAGATGATAAC 5

RESULT 10
US-11-217-529-77397/c
; Sequence 77397, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77397
; LENGTH: 351
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77397

Query Match      57.9%; Score 16.2; DB 7; Length 351;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AATTGGGTACAAGATGATACC 22
DB 33 AATTGGGTATAAGATGATAAC 13

RESULT 11
US-10-505-928-492
; Sequence 492, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 492
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-492

Query Match      57.9%; Score 16.2; DB 6; Length 3054;
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Best Local Similarity 85.7%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 GGTACAAGATGATACCTTCGT 27
DB 886 GTTGAAGATGATACCTTCGT 906

RESULT 12
US-11-217-529-82662
; Sequence 82662, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82662
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82662

Query Match 57.1%; Score 16; DB 7; Length 378;
Best Local Similarity 79.2%; Pred. No. 38;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TTGGGTACAAGATGATACCTTCGT 27
DB 211 TTGGATACAGATCATACCTTCGT 234

RESULT 13
US-10-953-349-3885/c
; Sequence 3885, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3885
; LENGTH: 1501
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3885

Query Match 57.1%; Score 16; DB 6; Length 1501;
Best Local Similarity 79.2%; Pred. No. 50;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 ATTGGGTACAAGATGATACCTTCG 26
DB 166 ATTCGGTAGAAGATGACTCCTTCG 143

RESULT 14
US-10-953-349-28833
; Sequence 28833, Application US/10953349

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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28833
; LENGTH: 1811
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-28833

Query Match 57.1%; Score 16; DB 6; Length 1811;
Best Local Similarity 79.2%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTT 24
DB 961 AAATTGGTTACAAAATCATAGCCT 984

RESULT 15
US-10-953-349-5704
; Sequence 5704, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5704
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5704

Query Match 57.1%; Score 16; DB 6; Length 1821;
Best Local Similarity 79.2%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAATTGGGTACAAGATGATACCTT 24
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 6	13	92.9	1758	3	US-09-598-419-336 Sequence 336, App
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C 8	13	92.9	2068	2	US-08-608-267-1 Sequence 1, Appli
C 9	13	92.9	2068	2	US-08-608-452-1 Sequence 1, Appli
C 10	13	92.9	2068	2	US-08-608-224-1 Sequence 1, Appli
C 11	13	92.9	2068	2	US-08-967-149-1 Sequence 1, Appli
C 12	13	92.9	4191	3	US-10-197-220-165 Sequence 165, App
C 13	13	92.9	5365	3	US-09-556-877-174 Sequence 174, App
C 14	13	92.9	5365	3	US-09-620-412C-174 Sequence 174, App
C 15	13	92.9	5365	3	US-09-598-419-174 Sequence 174, App
C 16	13	92.9	6735	3	US-08-961-527-104 Sequence 104, App
C 17	13	92.9	15164	3	US-09-949-016-11759 Sequence 11759, A
C 18	13	92.9	15165	3	US-09-949-016-15664 Sequence 15664, A
C 19	13	92.9	300402	3	US-09-949-016-13632 Sequence 13632, A
C 20	13	92.9	767677	3	US-09-949-016-12147 Sequence 12147, A
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104	12.4	88.6	15273	3	US-09-949-016-13341	Sequence 13341, A	c 177	12.4	88.6	818128	3	US-09-949-016-14549	Sequence 14549, A
c 105	12.4	88.6	17844	5	US-09-543-679A-2925	Sequence 2925, Ap	178	12.4	88.6	818128	3	US-09-949-016-14550	Sequence 14550, A
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c 110	12.4	88.6	36760	3	US-09-949-016-14021	Sequence 14021, A	c 183	12.4	88.6	818128	3	US-09-949-016-14552	Sequence 14552, A
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c 117	12.4	88.6	47420	3	US-09-949-016-15484	Sequence 15484, A	190	12.4	88.6	818128	3	US-09-949-016-14556	Sequence 14556, A
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c 145	12.4	88.6	151295	3	US-09-949-016-14568	Sequence 14568, A	c 218	12	85.7	324	4	US-09-533-539-2373	Sequence 2373, Ap
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245	12	85.7	601	3	US-09-949-016-196378	Sequence 196378,	318	12	85.7	73008	3	US-09-949-016-16326	Sequence 16326, A
c 246	12	85.7	601	3	US-09-949-016-202053	Sequence 202053,	c 319	12	85.7	74804	3	US-09-949-016-15118	Sequence 15118, A
c 247	12	85.7	601	3	US-09-949-016-202054	Sequence 202054,	320	12	85.7	77851	3	US-09-949-016-12508	Sequence 12508, A
248	12	85.7	768	3	US-09-540-236-909	Sequence 909, App	321	12	85.7	77867	3	US-09-949-016-13211	Sequence 13211, A
c 249	12	85.7	843	3	US-09-328-322-1259	Sequence 1259, Ap	322	12	85.7	77867	3	US-09-949-016-13212	Sequence 13212, A
c 250	12	85.7	861	3	US-09-902-540-4130	Sequence 4130, Ap	323	12	85.7	77940	3	US-09-949-016-12509	Sequence 12509, A
c 251	12	85.7	861	3	US-10-099-322-321	Sequence 321, App	c 324	12	85.7	83938	3	US-09-949-016-16068	Sequence 16068, A
c 252	12	85.7	877	3	US-09-636-215-769	Sequence 769, App	c 325	12	85.7	89268	3	US-09-949-016-12025	Sequence 12025, A
c 253	12	85.7	877	3	US-09-685-166A-769	Sequence 769, App	c 326	12	85.7	90544	3	US-09-949-016-11302	Sequence 11302, A
c 254	12	85.7	877	3	US-09-679-426-769	Sequence 769, App	c 327	12	85.7	95566	3	US-09-949-016-11877	Sequence 11877, A
c 255	12	85.7	877	3	US-09-759-143-769	Sequence 769, App	c 328	12	85.7	99370	3	US-09-949-016-12816	Sequence 12816, A
c 256	12	85.7	877	3	US-09-651-236-769	Sequence 769, App	c 329	12	85.7	99370	3	US-09-949-016-17540	Sequence 17540, A
c 257	12	85.7	877	3	US-09-657-279-769	Sequence 769, App	c 330	12	85.7	101894	3	US-09-949-016-12505	Sequence 12505, A
c 258	12	85.7	877	3	US-10-112-896-769	Sequence 769, App	c 331	12	85.7	103894	3	US-09-949-016-14450	Sequence 14450, A
c 259	12	85.7	877	5	US-10-144-678A-769	Sequence 769, App	c 332	12	85.7	105168	3	US-09-949-016-13296	Sequence 13296, A
c 260	12	85.7	929	3	US-09-533-559-7620	Sequence 7620, Ap	333	12	85.7	126237	3	US-09-949-016-16674	Sequence 16674, A
c 261	12	85.7	1092	3	US-09-902-340-3303	Sequence 3303, Ap	334	12	85.7	126237	3	US-09-949-016-16675	Sequence 16675, A
c 262	12	85.7	1170	5	US-09-974-300-1705	Sequence 1705, Ap	c 335	12	85.7	128723	3	US-09-949-016-17533	Sequence 17533, A
263	12	85.7	1192	4	US-10-099-322-17	Sequence 17, Appl	c 336	12	85.7	143155	3	US-09-949-016-11925	Sequence 11925, A
264	12	85.7	1192	4	US-09-880-107-3409	Sequence 3409, Ap	c 337	12	85.7	143164	3	US-09-949-016-14368	Sequence 14368, A
265	12	85.7	1192	4	US-10-044-564-17	Sequence 17, Appl	c 338	12	85.7	143173	3	US-09-949-016-14513	Sequence 14513, A
266	12	85.7	1245	3	US-09-354-123-7	Sequence 7, Appl	339	12	85.7	152331	3	US-09-128-155-16	Sequence 16, Appl
267	12	85.7	1260	3	US-09-328-322-272	Sequence 272, Appl	c 340	12	85.7	153642	3	US-09-949-016-12174	Sequence 12174, A
268	12	85.7	1503	4	US-09-605-703B-1765	Sequence 1765, Ap	c 341	12	85.7	153642	3	US-09-949-016-12174	Sequence 12174, A
269	12	85.7	1840	3	US-09-620-312B-320	Sequence 320, App	342	12	85.7	153643	3	US-09-949-016-15635	Sequence 15635, A
c 270	12	85.7	1980	3	US-09-543-681A-576	Sequence 576, App	c 343	12	85.7	153643	3	US-09-949-016-15635	Sequence 15635, A
c 271	12	85.7	2011	3	US-09-949-016-4326	Sequence 4326, Ap	c 344	12	85.7	172677	3	US-09-949-016-13444	Sequence 13444, A
c 272	12	85.7	2026	2	US-08-559-492-1	Sequence 1, Appl	345	12	85.7	172677	3	US-09-128-155-17	Sequence 17, Appl
c 273	12	85.7	2026	4	US-09-880-107-3669	Sequence 3669, Ap	346	12	85.7	177251	3	US-09-949-016-15841	Sequence 15841, A
c 274	12	85.7	2368	3	US-09-343-011B-3	Sequence 3, Appl	c 347	12	85.7	187136	3	US-09-949-016-17231	Sequence 17231, A
c 275	12	85.7	2461	4	US-09-880-107-2126	Sequence 2126, Ap	348	12	85.7	194790	3	US-09-949-016-15393	Sequence 15393, A
c 276	12	85.7	2664	3	US-09-540-236-991	Sequence 991, App	349	12	85.7	229354	3	US-09-705-400-64	Sequence 64, Appl
c 277	12	85.7	2759	4	US-09-784-340-1	Sequence 1, Appl	c 350	12	85.7	231129	3	US-09-949-016-16110	Sequence 16110, A
c 278	12	85.7	2765	3	US-10-104-047-528	Sequence 528, App	c 351	12	85.7	262923	3	US-09-949-016-11934	Sequence 11934, A
c 279	12	85.7	2956	3	US-09-710-279-3531	Sequence 3531, Ap	c 352	12	85.7	262923	3	US-09-596-002-41	Sequence 41, Appl
c 280	12	85.7	3116	3	US-09-710-279-3991	Sequence 3991, Ap	c 353	12	85.7	271134	3	US-09-949-016-12705	Sequence 12705, A
c 281	12	85.7	3335	3	US-10-104-047-522	Sequence 522, App	c 354	12	85.7	305491	3	US-09-949-016-17550	Sequence 17550, A
c 282	12	85.7	3488	3	US-08-930-285-12	Sequence 12, Appl	c 355	12	85.7	1082144	4	US-09-531-120-211	Sequence 211, App
c 283	12	85.7	3544	3	US-08-637-826A-11	Sequence 11, Appl	356	11.4	81.4	18	3	US-09-978-522-22	Sequence 22, Appl
c 284	12	85.7	3694	3	US-09-324-258-6	Sequence 6, Appl	c 357	11.4	81.4	19	3	US-09-978-522-22	Sequence 22, Appl
c 285	12	85.7	3881	3	US-09-710-279-3751	Sequence 3751, Ap	358	11.4	81.4	50	5	US-10-131-827-686	Sequence 686, App
c 286	12	85.7	3931	3	US-08-956-171B-342	Sequence 342, App	359	11.4	81.4	50	5	US-10-131-831-686	Sequence 686, App
c 287	12	85.7	3931	3	US-08-781-986A-342	Sequence 342, App	360	11.4	81.4	79	2	US-08-472-255A-141	Sequence 141, App
c 288	12	85.7	4315	2	US-08-781-802-1	Sequence 1, Appl	361	11.4	81.4	79	2	US-08-479-724A-141	Sequence 141, App
c 289	12	85.7	4315	3	US-08-694-078-1	Sequence 1, Appl	362	11.4	81.4	79	3	US-08-472-256B-141	Sequence 141, App
c 290	12	85.7	5362	2	US-08-853-310-3	Sequence 3, Appl	363	11.4	81.4	79	3	US-08-952-793-141	Sequence 141, App
c 291	12	85.7	5785	3	US-09-591-500A-1	Sequence 1, Appl	364	11.4	81.4	79	3	US-08-849-528-141	Sequence 141, App
c 292	12	85.7	10092	5	US-09-702-540-994	Sequence 994, App	365	11.4	81.4	92	3	FCT-US96-09455A-141	Sequence 51, Appl
c 293	12	85.7	10266	3	US-09-700-843-1	Sequence 1, Appl	c 366	11.4	81.4	92	3	US-08-433-522A-51	Sequence 51, Appl
c 294	12	85.7	13248	3	US-09-949-016-12024	Sequence 12024, A	c 367	11.4	81.4	92	3	US-09-135-166-51	Sequence 51, Appl
c 295	12	85.7	13248	3	US-09-949-016-14230	Sequence 14230, A	c 368	11.4	81.4	92	3	US-08-942-046-51	Sequence 51, Appl
c 296	12	85.7	16373	3	US-09-949-016-12820	Sequence 12820, A	c 369	11.4	81.4	148	3	US-09-313-294A-230	Sequence 230, App
c 297	12	85.7	16373	3	US-09-949-016-16897	Sequence 16897, A	c 370	11.4	81.4	182	3	US-09-513-999C-8394	Sequence 8394, App
c 298	12	85.7	17318	3	US-09-949-016-13817	Sequence 13817, A	c 371	11.4	81.4	242	3	US-08-602-145-12	Sequence 12, Appl
c 299	12	85.7	17639	3	US-09-902-540-1153	Sequence 1153, Ap	c 372	11.4	81.4	258	3	US-09-313-294A-2308	Sequence 2308, App
c 300	12	85.7	18925	3	US-09-949-016-14118	Sequence 14118, A	c 373	11.4	81.4	268	3	US-09-313-294A-2429	Sequence 2429, Ap
c 301	12	85.7	18926	3	US-09-949-016-11938	Sequence 11938, A	c 374	11.4	81.4	271	3	US-09-313-294A-2402	Sequence 2402, Ap
c 302	12	85.7	21296	3	US-09-949-016-14504	Sequence 14504, A	c 375	11.4	81.4	273	3	US-09-513-999C-26024	Sequence 26024, A
c 303	12	85.7	21296	3	US-09-949-016-14505	Sequence 14505, A	c 376	11.4	81.4	287	3	US-09-513-999C-13540	Sequence 13540, A
c 304	12	85.7	21296	3	US-09-949-016-15701	Sequence 15701, A	377	11.4	81.4	294	3	US-09-540-236-1328	Sequence 1328, Ap
c 305	12	85.7	21296	3	US-09-949-016-15702	Sequence 15702, A	378	11.4	81.4	295	3	US-09-533-559-1530	Sequence 1530, Ap
c 306	12	85.7	23091	3	US-09-902-540-1204	Sequence 1204, Ap	379	11.4	81.4	296	3	US-08-602-145-14	Sequence 14, Appl
c 307	12	85.7	24368	3	US-09-949-016-15050	Sequence 15050, A	380	11.4	81.4	300	4	US-09-297-648-2466	Sequence 2466, Ap
c 308	12	85.7	25131	3	US-09-949-016-12385	Sequence 12385, A	c 381	11.4	81.4	303	3	US-09-513-999C-9035	Sequence 9035, App
c 309	12	85.7	26138	3	US-09-949-016-13653	Sequence 13653, A	c 382	11.4	81.4	365	3	US-09-270-767-3712	Sequence 3712, Ap
c 310	12	85.7	26486	3	US-09-949-016-17407	Sequence 17407, A	c 383	11.4	81.4	365	3	US-09-270-767-18994	Sequence 18994, A
c 311	12	85.7	28843	3	US-09-949-016-17325	Sequence 17325, A	c 384	11.4	81.4	370	2	US-08-967-101-49	Sequence 49, Appl
c 312	12	85.7	31147	3	US-09-536-002-25	Sequence 25, Appl	c 385	11.4	81.4	370	2	US-08-952-541-49	Sequence 49, Appl
c 313	12	85.7	40219	3	US-09-949-016-15337	Sequence 15337, A	c 386	11.4	81.4	370	3	US-09-124-698-49	Sequence 49, Appl
c 314	12	85.7	52992	3	US-09-949-016-16105	Sequence 16105, A	c 387	11.4	81.4	370	3	US-09-127-480-49	Sequence 49, Appl
c 315	12	85.7	54270	3	US-09-949-016-16096	Sequence 16096, A	c 388	11.4	81.4	370	3	US-08-496-841C-49	Sequence 49, Appl

C 389	11.4	81.4	370	3	US-09-124-523-49	Sequence 49, Appl	462	11.4	81.4	601	3	US-09-949-016-21974	Sequence 21974, A
C 390	11.4	81.4	370	3	US-09-636-796A-49	Sequence 49, Appl	463	11.4	81.4	601	3	US-09-949-016-21975	Sequence 21975, A
C 391	11.4	81.4	370	3	US-08-431-048F-49	Sequence 49, Appl	464	11.4	81.4	601	3	US-09-949-016-21976	Sequence 21976, A
C 392	11.4	81.4	372	4	US-09-689-159A-49	Sequence 49, Appl	465	11.4	81.4	601	3	US-09-949-016-21977	Sequence 21977, A
C 393	11.4	81.4	377	2	US-08-967-101-53	Sequence 53, Appl	466	11.4	81.4	601	3	US-09-949-016-21978	Sequence 21978, A
C 394	11.4	81.4	377	2	US-08-967-101-53	Sequence 53, Appl	467	11.4	81.4	601	3	US-09-949-016-21979	Sequence 21979, A
C 395	11.4	81.4	377	3	US-09-124-698-53	Sequence 53, Appl	C 468	11.4	81.4	601	3	US-09-949-016-21980	Sequence 21980, A
C 396	11.4	81.4	377	3	US-09-127-480-53	Sequence 53, Appl	C 469	11.4	81.4	601	3	US-09-949-016-21981	Sequence 21981, A
C 397	11.4	81.4	377	3	US-08-496-841C-53	Sequence 53, Appl	C 470	11.4	81.4	601	3	US-09-949-016-21982	Sequence 21982, A
C 398	11.4	81.4	377	3	US-09-124-523-53	Sequence 53, Appl	C 471	11.4	81.4	601	3	US-09-949-016-21983	Sequence 21983, A
C 399	11.4	81.4	377	3	US-09-636-796A-53	Sequence 53, Appl	C 472	11.4	81.4	601	3	US-09-949-016-21984	Sequence 21984, A
C 400	11.4	81.4	377	3	US-08-431-048F-53	Sequence 53, Appl	C 473	11.4	81.4	601	3	US-09-949-016-21985	Sequence 21985, A
C 401	11.4	81.4	380	4	US-09-689-159A-53	Sequence 53, Appl	474	11.4	81.4	601	3	US-09-949-016-21986	Sequence 21986, A
C 402	11.4	81.4	386	2	US-08-967-101-52	Sequence 52, Appl	475	11.4	81.4	601	3	US-09-949-016-21987	Sequence 21987, A
C 403	11.4	81.4	386	2	US-08-967-101-52	Sequence 52, Appl	476	11.4	81.4	601	3	US-09-949-016-21988	Sequence 21988, A
C 404	11.4	81.4	386	3	US-09-124-698-52	Sequence 52, Appl	477	11.4	81.4	601	3	US-09-949-016-21989	Sequence 21989, A
C 405	11.4	81.4	386	3	US-09-127-480-52	Sequence 52, Appl	C 478	11.4	81.4	601	3	US-09-949-016-21990	Sequence 21990, A
C 406	11.4	81.4	386	3	US-08-496-841C-52	Sequence 52, Appl	C 479	11.4	81.4	601	3	US-09-949-016-21991	Sequence 21991, A
C 407	11.4	81.4	386	3	US-09-124-523-52	Sequence 52, Appl	C 480	11.4	81.4	601	3	US-09-949-016-21992	Sequence 21992, A
C 408	11.4	81.4	386	3	US-09-636-796A-52	Sequence 52, Appl	C 481	11.4	81.4	601	3	US-09-949-016-21993	Sequence 21993, A
C 409	11.4	81.4	386	3	US-08-431-048F-52	Sequence 52, Appl	C 482	11.4	81.4	601	3	US-09-949-016-21994	Sequence 21994, A
C 410	11.4	81.4	387	4	US-09-689-159A-52	Sequence 52, Appl	C 483	11.4	81.4	601	3	US-09-949-016-21995	Sequence 21995, A
C 411	11.4	81.4	390	3	US-09-107-532A-775	Sequence 52, Appl	484	11.4	81.4	601	3	US-09-949-016-21996	Sequence 21996, A
C 412	11.4	81.4	390	3	US-09-489-039A-3791	Sequence 3791, Ap	485	11.4	81.4	601	3	US-09-949-016-21997	Sequence 21997, A
C 413	11.4	81.4	400	3	US-09-513-999C-10479	Sequence 10479, A	486	11.4	81.4	601	3	US-09-949-016-21998	Sequence 21998, A
C 414	11.4	81.4	409	3	US-09-270-767-2687	Sequence 2687, Ap	487	11.4	81.4	601	3	US-09-949-016-21999	Sequence 21999, A
C 415	11.4	81.4	409	3	US-09-270-767-2687	Sequence 2687, Ap	488	11.4	81.4	601	3	US-09-949-016-22000	Sequence 22000, A
C 416	11.4	81.4	440	2	US-08-967-101-58	Sequence 58, Appl	489	11.4	81.4	601	3	US-09-949-016-22001	Sequence 22001, A
C 417	11.4	81.4	440	2	US-08-967-101-58	Sequence 58, Appl	490	11.4	81.4	601	3	US-09-949-016-22002	Sequence 22002, A
C 418	11.4	81.4	440	3	US-08-592-541-58	Sequence 58, Appl	491	11.4	81.4	601	3	US-09-949-016-22003	Sequence 22003, A
C 419	11.4	81.4	440	3	US-09-124-698-58	Sequence 58, Appl	492	11.4	81.4	601	3	US-09-949-016-22004	Sequence 22004, A
C 420	11.4	81.4	440	3	US-09-127-480-58	Sequence 58, Appl	493	11.4	81.4	601	3	US-09-949-016-22005	Sequence 22005, A
C 421	11.4	81.4	440	3	US-08-496-841C-58	Sequence 58, Appl	494	11.4	81.4	601	3	US-09-949-016-22006	Sequence 22006, A
C 422	11.4	81.4	440	3	US-09-124-523-58	Sequence 58, Appl	495	11.4	81.4	601	3	US-09-949-016-22007	Sequence 22007, A
C 423	11.4	81.4	440	3	US-09-636-796A-58	Sequence 58, Appl	496	11.4	81.4	601	3	US-09-949-016-22008	Sequence 22008, A
C 424	11.4	81.4	440	3	US-08-431-048F-58	Sequence 58, Appl	497	11.4	81.4	601	3	US-09-949-016-22009	Sequence 22009, A
C 425	11.4	81.4	442	3	US-09-689-159A-58	Sequence 58, Appl	C 498	11.4	81.4	601	3	US-09-949-016-22010	Sequence 22010, A
C 426	11.4	81.4	442	3	US-09-270-767-3123	Sequence 3123, Ap	C 499	11.4	81.4	601	3	US-09-949-016-22011	Sequence 22011, A
C 427	11.4	81.4	446	3	US-09-270-767-18405	Sequence 18405, A	C 500	11.4	81.4	601	3	US-09-949-016-22012	Sequence 22012, A
C 428	11.4	81.4	457	3	US-09-621-976-13229	Sequence 13229, A	C 501	11.4	81.4	601	3	US-09-949-016-22013	Sequence 22013, A
C 429	11.4	81.4	465	3	US-09-621-976-11119	Sequence 11119, A	C 502	11.4	81.4	601	3	US-09-949-016-22014	Sequence 22014, A
C 430	11.4	81.4	468	3	US-09-489-039A-3756	Sequence 3756, Ap	C 503	11.4	81.4	601	3	US-09-949-016-22015	Sequence 22015, A
C 431	11.4	81.4	468	3	US-09-270-767-17084	Sequence 17084, Ap	C 504	11.4	81.4	601	3	US-09-949-016-22016	Sequence 22016, A
C 432	11.4	81.4	477	3	US-09-313-294A-4870	Sequence 4870, Ap	C 505	11.4	81.4	601	3	US-09-949-016-22017	Sequence 22017, A
C 433	11.4	81.4	482	3	US-09-270-767-8390	Sequence 8390, Ap	C 506	11.4	81.4	601	3	US-09-949-016-22018	Sequence 22018, A
C 434	11.4	81.4	482	3	US-09-270-767-23672	Sequence 23672, A	C 507	11.4	81.4	601	3	US-09-949-016-22019	Sequence 22019, A
C 435	11.4	81.4	483	3	US-09-621-976-9241	Sequence 9241, Ap	C 508	11.4	81.4	601	3	US-09-949-016-22020	Sequence 22020, A
C 436	11.4	81.4	495	3	US-09-533-559-1725	Sequence 1725, Ap	C 509	11.4	81.4	601	3	US-09-949-016-22021	Sequence 22021, A
C 437	11.4	81.4	498	3	US-09-621-976-17779	Sequence 17779, Ap	C 510	11.4	81.4	601	3	US-09-949-016-22022	Sequence 22022, A
C 438	11.4	81.4	501	5	US-09-374-300-6752	Sequence 6752, Ap	C 511	11.4	81.4	601	3	US-09-949-016-22023	Sequence 22023, A
C 439	11.4	81.4	503	3	US-09-621-976-16499	Sequence 16499, A	C 512	11.4	81.4	601	3	US-09-949-016-22024	Sequence 22024, A
C 440	11.4	81.4	503	3	US-09-621-976-16500	Sequence 16500, A	C 513	11.4	81.4	601	3	US-09-949-016-22025	Sequence 22025, A
C 441	11.4	81.4	503	3	US-09-621-976-16501	Sequence 16501, A	C 514	11.4	81.4	601	3	US-09-949-016-22026	Sequence 22026, A
C 442	11.4	81.4	504	3	US-09-540-236-1375	Sequence 1375, Ap	C 515	11.4	81.4	601	3	US-09-949-016-22027	Sequence 22027, A
C 443	11.4	81.4	509	4	US-09-880-107-110	Sequence 110, App	C 516	11.4	81.4	601	3	US-09-949-016-22028	Sequence 22028, A
C 444	11.4	81.4	513	3	US-09-621-976-16497	Sequence 16497, A	C 517	11.4	81.4	601	3	US-09-949-016-22029	Sequence 22029, A
C 445	11.4	81.4	526	3	US-09-513-999C-15677	Sequence 15677, A	C 518	11.4	81.4	601	3	US-09-949-016-22030	Sequence 22030, A
C 446	11.4	81.4	528	3	US-09-949-016-3093	Sequence 3093, Ap	C 519	11.4	81.4	601	3	US-09-949-016-22031	Sequence 22031, A
C 447	11.4	81.4	529	3	US-09-949-016-2262	Sequence 2262, Ap	C 520	11.4	81.4	601	3	US-09-949-016-22032	Sequence 22032, A
C 448	11.4	81.4	531	4	US-09-880-107-137	Sequence 137, Appl	C 521	11.4	81.4	601	3	US-09-949-016-22033	Sequence 22033, A
C 449	11.4	81.4	535	3	US-09-770-509-1	Sequence 1, Appl	C 522	11.4	81.4	601	3	US-09-949-016-22034	Sequence 22034, A
C 450	11.4	81.4	540	3	US-09-489-039A-156	Sequence 156, App	C 523	11.4	81.4	601	3	US-09-949-016-22035	Sequence 22035, A
C 451	11.4	81.4	541	3	US-09-270-767-5356	Sequence 5356, Ap	C 524	11.4	81.4	601	3	US-09-949-016-22036	Sequence 22036, A
C 452	11.4	81.4	541	3	US-09-270-767-20638	Sequence 20638, A	C 525	11.4	81.4	601	3	US-09-949-016-22037	Sequence 22037, A
C 453	11.4	81.4	547	3	US-09-270-767-25948	Sequence 25948, A	C 526	11.4	81.4	601	3	US-09-949-016-22038	Sequence 22038, A
C 454	11.4	81.4	550	3	US-08-998-416-148	Sequence 148, App	C 527	11.4	81.4	601	3	US-09-949-016-22039	Sequence 22039, A
C 455	11.4	81.4	558	3	US-09-489-039A-6933	Sequence 6933, Ap	C 528	11.4	81.4	601	3	US-09-949-016-22040	Sequence 22040, A
C 456	11.4	81.4	582	5	US-09-974-300-5347	Sequence 5347, Ap	C 529	11.4	81.4	601	3	US-09-949-016-22041	Sequence 22041, A
C 457	11.4	81.4	584	5	US-09-974-300-608	Sequence 608, App	C 530	11.4	81.4	601	3	US-09-949-016-22042	Sequence 22042, A
C 458	11.4	81.4	586	3	US-09-533-559-1738	Sequence 1738, Ap	C 531	11.4	81.4	601	3	US-09-949-016-22043	Sequence 22043, A
C 459	11.4	81.4	588	5	US-09-974-300-4576	Sequence 4576, Ap	C 532	11.4	81.4	601	3	US-09-949-016-22044	Sequence 22044, A
C 460	11.4	81.4	593	5	US-09-974-300-4874	Sequence 4874, Ap	C 533	11.4	81.4	601	3	US-09-949-016-22045	Sequence 22045, A
C 461	11.4	81.4	601	3	US-09-949-016-18973	Sequence 18973, A	C 534	11.4	81.4	601	3	US-09-949-016-18974	Sequence 18974, A

535	11.4	81.4	601	3	US-09-949-016-157962	Sequence 157962,	c 608	11.4	81.4	859	3	US-09-044-604-2	Sequence 2, Appli
536	11.4	81.4	601	3	US-09-949-016-157963	Sequence 157963,	c 609	11.4	81.4	864	3	US-09-270-767-10692	Sequence 10692, A
c 537	11.4	81.4	601	3	US-09-949-016-160683	Sequence 160683,	610	11.4	81.4	873	3	US-09-513-990C-8465	Sequence 8465, Ap
538	11.4	81.4	601	3	US-09-949-016-160857	Sequence 160857,	611	11.4	81.4	882	3	US-09-949-016-3413	Sequence 3413, Ap
539	11.4	81.4	601	3	US-09-949-016-160858	Sequence 160858,	612	11.4	81.4	885	3	US-09-489-039A-5254	Sequence 5254, Ap
540	11.4	81.4	601	3	US-09-949-016-163274	Sequence 163274,	613	11.4	81.4	905	3	US-09-602-787A-325	Sequence 325, App
541	11.4	81.4	601	3	US-09-949-016-163275	Sequence 163275,	614	11.4	81.4	906	5	US-09-974-300-2335	Sequence 2335, Ap
c 542	11.4	81.4	601	3	US-09-949-016-155298	Sequence 165298,	c 615	11.4	81.4	924	3	US-09-991-181-508	Sequence 508, App
543	11.4	81.4	601	3	US-09-949-016-166376	Sequence 166376,	c 616	11.4	81.4	924	3	US-09-990-444-508	Sequence 508, App
544	11.4	81.4	601	3	US-09-949-016-169123	Sequence 169123,	c 617	11.4	81.4	924	3	US-09-997-333-508	Sequence 508, App
545	11.4	81.4	601	3	US-09-949-016-171724	Sequence 171724,	c 618	11.4	81.4	924	3	US-09-992-598-508	Sequence 508, App
c 546	11.4	81.4	601	3	US-09-949-016-172455	Sequence 172455,	c 619	11.4	81.4	924	4	US-09-989-735-508	Sequence 508, App
547	11.4	81.4	601	3	US-09-949-016-172547	Sequence 172547,	c 620	11.4	81.4	924	5	US-09-989-726-508	Sequence 508, App
548	11.4	81.4	601	3	US-09-949-016-172548	Sequence 172548,	c 621	11.4	81.4	924	5	US-09-997-514-508	Sequence 508, App
549	11.4	81.4	601	3	US-09-949-016-172549	Sequence 172549,	c 622	11.4	81.4	924	5	US-09-989-728-508	Sequence 508, App
c 550	11.4	81.4	601	3	US-09-949-016-173810	Sequence 173810,	c 623	11.4	81.4	924	5	US-09-997-343-508	Sequence 508, App
c 551	11.4	81.4	601	3	US-09-949-016-173811	Sequence 173811,	c 624	11.4	81.4	924	5	US-09-997-653-508	Sequence 508, App
c 552	11.4	81.4	601	3	US-09-949-016-173812	Sequence 173812,	c 625	11.4	81.4	924	5	US-09-989-293A-508	Sequence 508, App
c 553	11.4	81.4	601	3	US-09-949-016-174970	Sequence 174970,	c 626	11.4	81.4	939	3	US-09-949-002-113	Sequence 113, App
c 554	11.4	81.4	601	3	US-09-949-016-174983	Sequence 174983,	c 627	11.4	81.4	948	3	US-09-248-796A-1474	Sequence 1474, Ap
c 555	11.4	81.4	601	3	US-09-949-016-174996	Sequence 174996,	c 628	11.4	81.4	966	2	US-08-921-382-1	Sequence 1, Appli
c 556	11.4	81.4	601	3	US-09-949-016-179438	Sequence 179438,	c 629	11.4	81.4	966	3	US-09-386-380-1	Sequence 1, Appli
c 557	11.4	81.4	601	3	US-09-949-016-179439	Sequence 179439,	c 630	11.4	81.4	991	3	US-09-149-476-175	Sequence 175, App
558	11.4	81.4	601	3	US-09-949-016-179447	Sequence 179447,	631	11.4	81.4	1001	3	US-09-641-638-260	Sequence 260, App
c 559	11.4	81.4	601	3	US-09-949-016-181312	Sequence 181312,	632	11.4	81.4	1001	3	US-09-671-317-427	Sequence 427, App
c 560	11.4	81.4	601	3	US-09-949-016-181349	Sequence 181349,	633	11.4	81.4	1001	3	US-10-170-097-260	Sequence 260, App
c 561	11.4	81.4	601	3	US-09-949-016-181386	Sequence 181386,	634	11.4	81.4	1008	3	US-09-533-553-2485	Sequence 2485, Ap
562	11.4	81.4	601	3	US-09-949-016-181632	Sequence 181632,	635	11.4	81.4	1020	3	US-09-710-279-1693	Sequence 1693, Ap
563	11.4	81.4	601	3	US-09-949-016-184495	Sequence 184495,	636	11.4	81.4	1038	2	US-08-134-570-13	Sequence 13, Appl
564	11.4	81.4	601	3	US-09-949-016-184496	Sequence 184496,	637	11.4	81.4	1041	3	US-09-134-001C-2359	Sequence 2359, Ap
565	11.4	81.4	601	3	US-09-949-016-184497	Sequence 184497,	638	11.4	81.4	1053	3	US-09-248-796A-5854	Sequence 5854, Ap
566	11.4	81.4	601	3	US-09-949-016-188302	Sequence 188302,	639	11.4	81.4	1059	3	US-09-328-352-2355	Sequence 2355, Ap
c 567	11.4	81.4	601	3	US-09-949-016-188367	Sequence 188367,	640	11.4	81.4	1078	3	US-09-543-681A-854	Sequence 854, App
c 568	11.4	81.4	601	3	US-09-949-016-188368	Sequence 188368,	641	11.4	81.4	1088	5	US-09-974-300-703	Sequence 703, App
c 569	11.4	81.4	601	3	US-09-949-016-194160	Sequence 194160,	642	11.4	81.4	1122	3	US-09-614-221A-61	Sequence 61, Appl
570	11.4	81.4	601	3	US-09-949-016-197805	Sequence 197805,	643	11.4	81.4	1122	3	US-09-270-767-10529	Sequence 10529, A
571	11.4	81.4	601	3	US-09-949-016-197852	Sequence 197852,	644	11.4	81.4	1160	3	US-09-153-310-41	Sequence 41, Appl
572	11.4	81.4	601	3	US-09-949-016-197852	Sequence 197852,	645	11.4	81.4	1185	3	US-09-248-796A-6620	Sequence 6620, Ap
c 573	11.4	81.4	601	3	US-09-949-016-198633	Sequence 198633,	646	11.4	81.4	1188	3	US-09-362-842-5	Sequence 5, Appli
c 574	11.4	81.4	601	3	US-09-949-016-198634	Sequence 198634,	647	11.4	81.4	1218	3	US-09-328-352-223	Sequence 223, App
c 575	11.4	81.4	601	3	US-09-949-016-202835	Sequence 202835,	648	11.4	81.4	1248	3	US-09-902-540-2311	Sequence 2311, Ap
c 576	11.4	81.4	601	3	US-09-949-016-204054	Sequence 204054,	c 649	11.4	81.4	1251	2	US-08-851-088-5	Sequence 5, Appli
c 577	11.4	81.4	601	3	US-09-949-016-204055	Sequence 204055,	c 650	11.4	81.4	1259	3	US-09-902-540-88	Sequence 88, Appl
c 578	11.4	81.4	601	3	US-09-949-016-204056	Sequence 204056,	c 651	11.4	81.4	1266	3	US-09-328-352-3014	Sequence 3014, Ap
c 579	11.4	81.4	601	3	US-09-949-016-204863	Sequence 204863,	652	11.4	81.4	1313	3	US-09-035-648-22	Sequence 22, Appl
c 580	11.4	81.4	601	3	US-09-949-016-204864	Sequence 204864,	653	11.4	81.4	1313	3	US-09-001-951-22	Sequence 22, Appl
581	11.4	81.4	601	3	US-09-949-002-913	Sequence 913, App	654	11.4	81.4	1313	3	US-08-818-825-22	Sequence 13, Appl
582	11.4	81.4	601	3	US-09-949-002-914	Sequence 914, App	c 655	11.4	81.4	1328	3	US-08-930-285-13	Sequence 2, Appli
c 583	11.4	81.4	601	3	US-09-949-002-1109	Sequence 1109, Ap	c 656	11.4	81.4	1371	3	US-09-350-753-3	Sequence 3, Appli
c 584	11.4	81.4	601	3	US-09-949-002-1649	Sequence 1649, Ap	c 657	11.4	81.4	1380	3	US-09-582-779A-1	Sequence 1, Appli
c 585	11.4	81.4	601	3	US-09-949-002-3922	Sequence 3922, Ap	658	11.4	81.4	1386	3	US-09-543-681A-1519	Sequence 1519, Ap
c 586	11.4	81.4	601	3	US-09-949-002-5280	Sequence 5280, Ap	c 659	11.4	81.4	1419	3	US-09-270-767-30657	Sequence 30657, A
c 587	11.4	81.4	601	3	US-09-949-002-5281	Sequence 5281, Ap	c 660	11.4	81.4	1422	3	US-09-134-000C-2035	Sequence 2035, A
c 588	11.4	81.4	601	3	US-09-949-002-5657	Sequence 5657, Ap	c 661	11.4	81.4	1440	3	US-09-543-681A-684	Sequence 684, App
c 589	11.4	81.4	601	3	US-09-949-002-5869	Sequence 5869, Ap	662	11.4	81.4	1475	3	US-09-244-805-13	Sequence 13, Appl
590	11.4	81.4	606	3	US-09-918-686-9	Sequence 9, Appli	663	11.4	81.4	1494	3	US-09-710-279-2811	Sequence 2811, Ap
591	11.4	81.4	618	3	US-09-710-279-3019	Sequence 3019, Ap	664	11.4	81.4	1497	3	US-09-328-352-880	Sequence 880, App
592	11.4	81.4	627	3	US-09-134-001C-1295	Sequence 1295, Ap	665	11.4	81.4	1515	3	US-09-902-540-9184	Sequence 9184, Ap
c 594	11.4	81.4	645	3	US-09-328-352-661	Sequence 661, App	666	11.4	81.4	1534	2	US-07-973-431B-2	Sequence 2, Appli
c 595	11.4	81.4	657	3	US-09-620-312D-543	Sequence 543, App	c 667	11.4	81.4	1539	2	US-08-899-811-22	Sequence 22, Appl
596	11.4	81.4	675	3	US-09-328-352-2490	Sequence 2490, Ap	668	11.4	81.4	1608	2	US-08-424-224-1	Sequence 1, Appli
c 597	11.4	81.4	678	3	US-09-533-559-4614	Sequence 4614, Ap	c 670	11.4	81.4	1652	3	US-08-726-214-17	Sequence 17, Appl
598	11.4	81.4	684	3	US-09-134-000C-2674	Sequence 2674, Ap	671	11.4	81.4	1683	3	US-09-976-594-861	Sequence 861, App
c 599	11.4	81.4	705	3	US-09-297-648-2897	Sequence 2897, Ap	c 672	11.4	81.4	1686	3	US-09-799-451-327	Sequence 327, App
c 600	11.4	81.4	715	3	US-09-533-559-4664	Sequence 4664, Ap	c 673	11.4	81.4	1723	2	US-08-804-699-1	Sequence 1, Appli
c 601	11.4	81.4	742	2	US-08-966-316-2	Sequence 2, Appli	674	11.4	81.4	1723	3	US-09-248-796A-391	Sequence 391, App
c 602	11.4	81.4	759	3	US-09-172-469B-1	Sequence 1, Appli	675	11.4	81.4	1784	2	US-08-808-931-19	Sequence 19, Appl
c 603	11.4	81.4	765	4	US-09-297-648-4411	Sequence 4411, Ap	676	11.4	81.4	1784	3	US-08-808-323-19	Sequence 19, Appl
c 604	11.4	81.4	781	4	US-09-297-648-3565	Sequence 3565, Ap	677	11.4	81.4	1784	3	US-09-050-603A-19	Sequence 19, Appl
c 605	11.4	81.4	840	3	US-09-724-623-37	Sequence 37, Appl	678	11.4	81.4	1784	3	US-09-102-420B-19	Sequence 19, Appl
c 606	11.4	81.4	840	3	US-10-288-930-37	Sequence 37, Appl	679	11.4	81.4	1784	3	US-09-497-698-19	Sequence 19, Appl
c 607	11.4	81.4	858	3	US-10-002-344A-66	Sequence 66, Appl	680	11.4	81.4	1784	3	US-09-730-525-19	Sequence 19, Appl

c 681	11.4	81.4	1800	2	US-08-366-783-1	Sequence 1, Appli	754	11.4	81.4	2682	3	US-09-949-016-5604	Sequence 5604, Ap
c 682	11.4	81.4	1800	2	US-08-313-098A-1	Sequence 1, Appli	755	11.4	81.4	2688	3	US-08-458-434A-3	Sequence 3, Appli
c 683	11.4	81.4	1800	2	US-08-846-021A-1	Sequence 1, Appli	756	11.4	81.4	2690	3	US-09-949-016-298	Sequence 298, App
c 684	11.4	81.4	1800	3	US-09-897-425-1	Sequence 1, Appli	757	11.4	81.4	2695	3	US-09-927-811D-8	Sequence 8, Appli
c 685	11.4	81.4	1800	3	US-09-893-525-1	Sequence 1, Appli	c 758	11.4	81.4	2709	3	US-09-313-275A-12	Sequence 12, Appl
c 686	11.4	81.4	1854	3	US-09-724-864-29	Sequence 29, Appl	c 759	11.4	81.4	2709	3	US-09-707-167-12	Sequence 12, Appl
c 687	11.4	81.4	1859	3	US-07-861-458C-1	Sequence 1, Appli	c 760	11.4	81.4	2720	3	US-10-012-231A-11	Sequence 11, Appl
c 688	11.4	81.4	1861	3	US-10-104-047-1707	Sequence 1707, Ap	c 761	11.4	81.4	2720	3	US-10-015-389A-11	Sequence 11, Appl
c 689	11.4	81.4	1902	2	US-09-258-257-1	Sequence 1, Appli	c 762	11.4	81.4	2720	3	US-10-006-768A-11	Sequence 11, Appl
c 690	11.4	81.4	1902	2	US-09-258-371-1	Sequence 1, Appli	c 763	11.4	81.4	2720	3	US-10-015-671A-11	Sequence 11, Appl
c 691	11.4	81.4	1902	3	US-08-569-721A-1	Sequence 1, Appli	c 764	11.4	81.4	2720	3	US-10-015-393A-11	Sequence 11, Appl
c 692	11.4	81.4	1902	3	US-08-751-230-1	Sequence 1, Appli	c 765	11.4	81.4	2720	3	US-10-011-833A-11	Sequence 11, Appl
c 693	11.4	81.4	1902	3	US-09-499-082-1	Sequence 1, Appli	c 766	11.4	81.4	2720	3	US-10-006-041A-11	Sequence 11, Appl
c 694	11.4	81.4	1902	3	US-09-358-372-1	Sequence 1, Appli	c 767	11.4	81.4	2720	3	US-10-012-064A-11	Sequence 11, Appl
c 695	11.4	81.4	1902	3	US-09-532-868-1	Sequence 1, Appli	c 768	11.4	81.4	2720	4	US-10-013-392A-11	Sequence 11, Appl
c 696	11.4	81.4	1903	3	US-09-927-811D-6	Sequence 6, Appli	c 769	11.4	81.4	2720	5	US-10-011-795B-11	Sequence 11, Appl
c 697	11.4	81.4	1939	3	US-09-949-016-2082	Sequence 2082, Ap	c 770	11.4	81.4	2720	5	US-10-015-386A-11	Sequence 11, Appl
c 698	11.4	81.4	1942	3	US-09-949-016-1029	Sequence 1029, Ap	c 771	11.4	81.4	2720	5	US-10-012-121A-11	Sequence 11, Appl
c 699	11.4	81.4	1947	3	US-09-489-847-26	Sequence 26, Appl	c 772	11.4	81.4	2720	5	US-10-006-485A-11	Sequence 11, Appl
c 700	11.4	81.4	1974	3	US-08-785-455-1	Sequence 1, Appli	c 773	11.4	81.4	2720	5	US-10-006-746A-11	Sequence 11, Appl
c 701	11.4	81.4	1974	4	US-09-302-024-1	Sequence 1, Appli	c 774	11.4	81.4	2720	5	US-10-012-752A-11	Sequence 11, Appl
c 702	11.4	81.4	1998	3	US-09-280-116-222	Sequence 22, App	c 775	11.4	81.4	2720	5	US-10-017-253A-11	Sequence 11, Appl
c 703	11.4	81.4	2031	3	US-08-583-110-1598	Sequence 1598, Ap	c 776	11.4	81.4	2720	5	US-10-015-519A-11	Sequence 11, Appl
c 704	11.4	81.4	2039	4	US-09-605-703B-2207	Sequence 2207, Ap	c 777	11.4	81.4	2720	5	US-10-015-715A-11	Sequence 11, Appl
c 705	11.4	81.4	2043	3	US-09-107-433-1321	Sequence 1321, Ap	c 778	11.4	81.4	2720	5	US-10-007-236A-11	Sequence 11, Appl
c 706	11.4	81.4	2044	2	US-10-094-749-111	Sequence 111, App	c 779	11.4	81.4	2733	2	US-08-846-021A-6	Sequence 6, Appli
c 707	11.4	81.4	2061	2	US-09-258-371-9	Sequence 9, Appli	c 780	11.4	81.4	2733	3	US-09-897-425-6	Sequence 6, Appli
c 708	11.4	81.4	2061	3	US-08-751-230-9	Sequence 9, Appli	c 781	11.4	81.4	2733	3	US-09-893-525-6	Sequence 6, Appli
c 709	11.4	81.4	2061	3	US-09-499-082-9	Sequence 9, Appli	c 782	11.4	81.4	2826	3	US-10-104-047-1128	Sequence 1128, Ap
c 710	11.4	81.4	2061	3	US-09-258-372-9	Sequence 9, Appli	c 783	11.4	81.4	2916	3	US-09-814-915A-31	Sequence 31, Appl
c 711	11.4	81.4	2061	3	US-09-006-783A-2	Sequence 2, Appli	c 784	11.4	81.4	2916	3	US-09-566-921-84	Sequence 84, Appl
c 712	11.4	81.4	2061	3	US-09-159-871-1	Sequence 1, Appli	c 785	11.4	81.4	3043	3	US-09-540-236-1265	Sequence 1265, Ap
c 713	11.4	81.4	2061	3	US-09-532-868-9	Sequence 9, Appli	c 786	11.4	81.4	3066	3	US-09-086-912-1	Sequence 1, Appli
c 714	11.4	81.4	2080	3	US-10-003-392-1	Sequence 1, Appli	c 787	11.4	81.4	3066	3	US-09-203-453-1	Sequence 1, Appli
c 715	11.4	81.4	2090	4	US-10-094-749-1168	Sequence 1168, Ap	c 788	11.4	81.4	3066	3	US-09-900-236-1	Sequence 1, Appli
c 716	11.4	81.4	2098	4	US-10-094-749-1336	Sequence 1336, Ap	c 789	11.4	81.4	3066	3	US-10-256-899-1	Sequence 1, Appli
c 717	11.4	81.4	2115	2	US-08-767-026-3	Sequence 3, Appli	c 790	11.4	81.4	3066	3	US-10-439-789-1	Sequence 1, Appli
c 718	11.4	81.4	2115	3	US-09-319-275A-3	Sequence 3, Appli	c 791	11.4	81.4	3076	2	US-09-205-144-1	Sequence 1, Appli
c 719	11.4	81.4	2115	3	US-09-707-167-3	Sequence 3, Appli	c 792	11.4	81.4	3076	2	US-09-814-915A-11	Sequence 11, Appl
c 720	11.4	81.4	2136	3	US-09-949-016-2970	Sequence 2970, Ap	c 793	11.4	81.4	3116	3	US-10-104-047-434	Sequence 434, App
c 721	11.4	81.4	2136	3	US-09-949-016-2971	Sequence 2971, Ap	c 794	11.4	81.4	3138	3	US-10-144-138-15	Sequence 15, Appl
c 722	11.4	81.4	2149	2	US-08-784-651-3	Sequence 3, Appli	c 795	11.4	81.4	3165	3	US-09-949-016-160	Sequence 160, App
c 723	11.4	81.4	2157	3	US-09-540-236-833	Sequence 833, App	c 796	11.4	81.4	3291	3	US-09-710-279-3691	Sequence 3691, Ap
c 724	11.4	81.4	2161	3	US-09-254-504-10	Sequence 10, Appl	c 797	11.4	81.4	3291	3	US-09-949-016-4658	Sequence 4658, Ap
c 725	11.4	81.4	2166	3	US-08-697-826A-12	Sequence 12, Appl	c 798	11.4	81.4	3309	3	US-09-710-279-3844	Sequence 3844, Ap
c 726	11.4	81.4	2193	3	US-09-107-532B-1098	Sequence 1098, Ap	c 799	11.4	81.4	3312	3	US-09-710-279-4308	Sequence 4308, Ap
c 727	11.4	81.4	2277	3	US-09-134-001C-1751	Sequence 1751, Ap	c 800	11.4	81.4	3314	3	US-09-949-016-836	Sequence 836, App
c 728	11.4	81.4	2288	2	US-08-568-459A-5	Sequence 5, Appli	c 801	11.4	81.4	3315	3	US-09-710-279-4363	Sequence 4363, Ap
c 729	11.4	81.4	2288	2	US-08-487-826B-5	Sequence 5, Appli	c 802	11.4	81.4	3341	2	US-08-868-577-18	Sequence 18, Appl
c 730	11.4	81.4	2288	3	US-09-210-288-5	Sequence 5, Appli	c 803	11.4	81.4	3341	3	US-09-207-914-18	Sequence 18, Appl
c 731	11.4	81.4	2288	3	US-10-153-273-5	Sequence 5, Appli	c 804	11.4	81.4	3453	3	US-09-023-655-1323	Sequence 1323, Ap
c 732	11.4	81.4	2312	3	US-09-356-806-114	Sequence 114, App	c 805	11.4	81.4	3573	3	US-09-710-279-3988	Sequence 3988, Ap
c 733	11.4	81.4	2335	3	US-10-104-047-748	Sequence 748, App	c 806	11.4	81.4	3573	3	US-09-949-016-5007	Sequence 5007, Ap
c 734	11.4	81.4	2468	2	US-07-779-049-2	Sequence 2, Appli	c 807	11.4	81.4	3585	3	US-09-270-767-14479	Sequence 14479, A
c 735	11.4	81.4	2468	2	US-08-080-240-2	Sequence 2, Appli	c 808	11.4	81.4	3629	3	US-09-328-352-2640	Sequence 2640, Ap
c 736	11.4	81.4	2499	4	US-10-094-749-207	Sequence 207, App	c 809	11.4	81.4	3724	3	US-09-710-279-3675	Sequence 3675, Ap
c 737	11.4	81.4	2517	3	US-09-712-363-4	Sequence 4, Appli	c 810	11.4	81.4	3778	3	US-09-799-451-160	Sequence 160, App
c 738	11.4	81.4	2520	3	US-09-929-612A-3	Sequence 3, Appli	c 811	11.4	81.4	3806	3	US-09-710-279-4166	Sequence 4166, Ap
c 739	11.4	81.4	2563	3	US-09-016-434-1076	Sequence 1076, Ap	c 812	11.4	81.4	3878	3	US-10-101-464A-950	Sequence 950, App
c 740	11.4	81.4	2563	3	US-09-023-655-894	Sequence 894, App	c 813	11.4	81.4	3888	3	US-10-101-464A-950	Sequence 950, App
c 741	11.4	81.4	2566	4	US-10-094-749-477	Sequence 477, App	c 814	11.4	81.4	3888	3	US-09-897-425-42	Sequence 42, Appl
c 742	11.4	81.4	2601	3	US-08-569-749-3	Sequence 3, Appli	c 815	11.4	81.4	3913	3	US-09-897-425-45	Sequence 45, Appl
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c 745	11.4	81.4	2601	3	US-10-334-717-3	Sequence 3, Appli	c 818	11.4	81.4	4008	3	US-08-726-214-3	Sequence 3, Appli
c 746	11.4	81.4	2601	7	PCT-US96-12860-3	Sequence 3, Appli	c 819	11.4	81.4	4060	2	PCT-US95-11808-5	Sequence 5, Appli
c 747	11.4	81.4	2652	3	US-09-489-039A-2545	Sequence 2545, Ap	c 820	11.4	81.4	4060	2	US-08-308-949A-1	Sequence 1, Appli
c 748	11.4	81.4	2676	2	US-08-511-485-5	Sequence 5, Appli	c 821	11.4	81.4	4122	3	US-09-873-737A-3	Sequence 3, Appli
c 749	11.4	81.4	2676	3	US-09-201-936-5	Sequence 5, Appli	c 822	11.4	81.4	4376	3	US-09-949-016-1777	Sequence 1777, Ap
c 750	11.4	81.4	2676	3	US-09-011-936-5	Sequence 5, Appli	c 823	11.4	81.4	4407	7	US-10-200-012-15	Sequence 15, Appl
c 751	11.4	81.4	2676	3	US-09-672-717-220	Sequence 220, App	c 824	11.4	81.4	4456	3	PCT-US93-05701-1	Sequence 1, Appli
c 752	11.4	81.4	2676	3	US-09-201-932-5	Sequence 5, Appli	c 825	11.4	81.4	4522	7	US-08-321-686B-1	Sequence 1, Appli
c 753	11.4	81.4	2676	4	US-09-654-743-5	Sequence 5, Appli	c 826	11.4	81.4	4529	3	PCT-US93-06251-22	Sequence 22, Appl
												US-09-949-016-14004	Sequence 14004, A

c 827	11.4	81.4	4545	3	US-09-897-425-53	Sequence 53, Appl	c 900	11.4	81.4	7194	4	US-10-428-826-76	Sequence 76, Appl
c 828	11.4	81.4	4546	3	US-09-897-425-50	Sequence 50, Appl	901	11.4	81.4	7243	3	US-09-949-016-5315	Sequence 5315, Ap
c 829	11.4	81.4	4628	3	US-09-949-016-5298	Sequence 5298, Ap	902	11.4	81.4	7410	3	US-09-973-278-748	Sequence 748, App
c 830	11.4	81.4	5100	2	US-08-164-292B-15	Sequence 15, Appl	903	11.4	81.4	7421	3	US-09-973-278-749	Sequence 749, App
c 831	11.4	81.4	5100	2	US-08-164-292B-17	Sequence 17, Appl	c 904	11.4	81.4	7453	3	US-09-949-016-16259	Sequence 16259, A
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c 833	11.4	81.4	5100	2	US-08-164-292B-21	Sequence 21, Appl	c 906	11.4	81.4	7765	3	US-09-949-016-13824	Sequence 13824, A
c 834	11.4	81.4	5100	2	US-08-164-292B-23	Sequence 23, Appl	c 907	11.4	81.4	7780	3	US-09-632-033B-2	Sequence 2, Appli
c 835	11.4	81.4	5100	2	US-08-164-292B-25	Sequence 25, Appl	c 908	11.4	81.4	7791	3	US-09-949-016-13900	Sequence 13900, A
c 836	11.4	81.4	5100	2	US-08-845-623-15	Sequence 15, Appl	c 909	11.4	81.4	7833	2	US-08-074-879-9	Sequence 9, Appli
c 837	11.4	81.4	5100	3	US-08-845-623-17	Sequence 17, Appl	c 910	11.4	81.4	7833	2	US-08-468-057A-9	Sequence 9, Appli
c 838	11.4	81.4	5100	3	US-08-845-623-19	Sequence 19, Appl	c 911	11.4	81.4	7912	3	US-09-949-016-3804	Sequence 3804, Ap
c 839	11.4	81.4	5100	3	US-08-845-623-21	Sequence 21, Appl	c 912	11.4	81.4	7912	3	US-09-632-033B-1	Sequence 1, Appli
c 840	11.4	81.4	5100	3	US-08-845-623-23	Sequence 23, Appl	c 913	11.4	81.4	7948	3	US-09-949-016-17596	Sequence 17596, A
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c 842	11.4	81.4	5100	3	US-08-815-927-15	Sequence 15, Appl	c 915	11.4	81.4	9132	3	US-09-949-016-13070	Sequence 13070, A
c 843	11.4	81.4	5100	3	US-08-815-927-17	Sequence 17, Appl	c 916	11.4	81.4	9139	3	US-09-322-478-22	Sequence 22, Appl
c 844	11.4	81.4	5100	3	US-08-815-927-19	Sequence 19, Appl	c 917	11.4	81.4	9139	3	US-09-586-106D-22	Sequence 22, Appl
c 845	11.4	81.4	5100	3	US-08-815-927-21	Sequence 21, Appl	c 918	11.4	81.4	9139	3	US-10-799-870-22	Sequence 22, Appl
c 846	11.4	81.4	5100	3	US-08-815-927-23	Sequence 23, Appl	c 919	11.4	81.4	9299	3	US-08-458-434A-7	Sequence 7, Appli
c 847	11.4	81.4	5100	3	US-08-815-927-25	Sequence 25, Appl	c 920	11.4	81.4	9301	3	US-09-449-218D-18	Sequence 18, Appl
c 848	11.4	81.4	5100	3	US-09-103-330-15	Sequence 15, Appl	c 921	11.4	81.4	9301	3	US-09-668-529A-18	Sequence 18, Appl
c 849	11.4	81.4	5100	3	US-09-103-330-17	Sequence 17, Appl	c 922	11.4	81.4	9301	3	US-09-668-037A-18	Sequence 18, Appl
c 850	11.4	81.4	5100	3	US-09-103-330-19	Sequence 19, Appl	c 923	11.4	81.4	9301	3	US-09-668-021-18	Sequence 18, Appl
c 851	11.4	81.4	5100	3	US-09-103-330-21	Sequence 21, Appl	c 924	11.4	81.4	9556	3	US-09-902-540-982	Sequence 982, App
c 852	11.4	81.4	5100	3	US-09-103-330-23	Sequence 23, Appl	c 925	11.4	81.4	10091	3	US-09-058-483-37	Sequence 34, Appl
c 853	11.4	81.4	5100	3	US-09-103-330-25	Sequence 25, Appl	c 926	11.4	81.4	10597	3	US-09-949-016-13766	Sequence 13766, A
c 854	11.4	81.4	5100	3	US-09-435-242-15	Sequence 15, Appl	c 927	11.4	81.4	11225	10	5182210-9	Patent No. 5182210
c 855	11.4	81.4	5100	3	US-09-435-242-17	Sequence 17, Appl	c 928	11.4	81.4	11271	3	US-08-956-171E-11	Sequence 11, Appl
c 856	11.4	81.4	5100	3	US-09-435-242-19	Sequence 19, Appl	c 929	11.4	81.4	11271	3	US-08-781-986A-11	Sequence 11, Appl
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c 858	11.4	81.4	5100	3	US-09-435-242-23	Sequence 23, Appl	c 931	11.4	81.4	11464	3	US-08-991-840A-2	Sequence 2, Appli
c 859	11.4	81.4	5100	3	US-09-435-242-25	Sequence 25, Appl	c 932	11.4	81.4	12626	3	US-09-949-003-685	Sequence 685, App
c 860	11.4	81.4	5100	5	US-10-046-938-15	Sequence 15, Appl	c 933	11.4	81.4	12752	2	US-08-459-146-1	Sequence 1, Appli
c 861	11.4	81.4	5100	5	US-10-046-938-17	Sequence 17, Appl	c 934	11.4	81.4	12752	2	US-08-459-065-1	Sequence 1, Appli
c 862	11.4	81.4	5100	5	US-10-046-938-19	Sequence 19, Appl	c 935	11.4	81.4	14094	3	US-09-949-016-14093	Sequence 14093, A
c 863	11.4	81.4	5100	5	US-10-046-938-21	Sequence 21, Appl	c 936	11.4	81.4	15393	3	US-09-453-702B-191	Sequence 191, App
c 864	11.4	81.4	5100	5	US-10-046-938-23	Sequence 23, Appl	c 937	11.4	81.4	15393	3	US-10-114-170-191	Sequence 191, App
c 865	11.4	81.4	5100	5	US-10-046-938-25	Sequence 25, Appl	c 938	11.4	81.4	15420	3	US-09-601-326-54	Sequence 54, Appl
c 866	11.4	81.4	5134	3	US-09-853-450-46	Sequence 46, Appl	c 939	11.4	81.4	15420	4	US-10-428-826-54	Sequence 54, Appl
c 867	11.4	81.4	5191	5	US-09-543-679A-2556	Sequence 2556, Ap	c 940	11.4	81.4	16207	3	US-09-949-016-16747	Sequence 16747, A
c 868	11.4	81.4	5307	3	US-10-028-056-2	Sequence 2, Appli	c 941	11.4	81.4	16236	3	US-09-949-016-16298	Sequence 16298, A
c 869	11.4	81.4	5418	3	US-09-893-525-38	Sequence 38, Appl	c 942	11.4	81.4	16344	3	US-09-949-016-16034	Sequence 16034, A
c 870	11.4	81.4	5521	3	US-08-975-762-48	Sequence 48, Appl	c 943	11.4	81.4	16716	3	US-09-949-016-17060	Sequence 17060, A
c 871	11.4	81.4	5521	3	US-09-295-028-48	Sequence 48, Appl	c 944	11.4	81.4	17488	3	US-09-949-016-15574	Sequence 15574, A
c 872	11.4	81.4	5521	3	US-09-106-582-48	Sequence 48, Appl	c 945	11.4	81.4	17930	3	US-09-949-016-11902	Sequence 11902, A
c 873	11.4	81.4	5521	3	US-09-159-469-48	Sequence 48, Appl	c 946	11.4	81.4	18048	3	US-09-949-016-12363	Sequence 12363, A
c 874	11.4	81.4	5521	3	US-09-693-542-48	Sequence 48, Appl	c 947	11.4	81.4	18049	3	US-09-949-016-16235	Sequence 16235, A
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c 876	11.4	81.4	5535	2	US-08-089-758A-4	Sequence 4, Appli	c 949	11.4	81.4	18351	3	US-09-949-016-16749	Sequence 16749, A
c 877	11.4	81.4	5535	2	US-08-421-754-1	Sequence 1, Appli	c 950	11.4	81.4	18351	3	US-09-949-016-17450	Sequence 17450, A
c 878	11.4	81.4	5535	2	US-08-421-754-4	Sequence 4, Appli	c 951	11.4	81.4	18494	3	US-09-949-016-15366	Sequence 15366, A
c 879	11.4	81.4	5535	2	US-08-421-791-1	Sequence 1, Appli	c 952	11.4	81.4	18534	3	US-09-949-016-13519	Sequence 13519, A
c 880	11.4	81.4	5535	2	US-08-421-791-4	Sequence 4, Appli	c 953	11.4	81.4	19167	3	US-09-949-016-12432	Sequence 12432, A
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c 882	11.4	81.4	5735	3	US-09-949-016-13169	Sequence 13169, A	c 955	11.4	81.4	20026	3	US-09-949-016-13147	Sequence 13147, A
c 883	11.4	81.4	6063	2	US-08-195-744-4	Sequence 4, Appli	c 956	11.4	81.4	20182	3	US-09-949-016-13240	Sequence 13240, A
c 884	11.4	81.4	6063	2	US-08-788-279-4	Sequence 4, Appli	c 957	11.4	81.4	20221	3	US-09-949-016-15366	Sequence 15366, A
c 885	11.4	81.4	6184	3	US-09-590-968B-1	Sequence 1, Appli	c 958	11.4	81.4	20537	3	US-09-949-016-12887	Sequence 12887, A
c 886	11.4	81.4	6595	3	US-09-142-108C-9	Sequence 9, Appli	c 959	11.4	81.4	20538	3	US-09-949-016-17052	Sequence 17052, A
c 887	11.4	81.4	6610	3	US-09-949-016-14835	Sequence 14835, A	c 960	11.4	81.4	20599	3	US-09-949-016-14477	Sequence 14477, A
c 888	11.4	81.4	6611	3	US-09-949-016-12357	Sequence 12357, A	c 961	11.4	81.4	20599	3	US-09-949-016-14478	Sequence 14478, A
c 889	11.4	81.4	6669	3	US-09-212-971-5	Sequence 5, Appli	c 962	11.4	81.4	21360	3	US-09-949-016-12857	Sequence 12857, A
c 890	11.4	81.4	6669	3	US-08-800-929A-5	Sequence 5, Appli	c 963	11.4	81.4	21361	3	US-09-949-016-16245	Sequence 16245, A
c 891	11.4	81.4	6669	3	US-09-617-053A-5	Sequence 5, Appli	c 964	11.4	81.4	21513	3	US-09-949-016-16695	Sequence 16695, A
c 892	11.4	81.4	6669	3	US-09-672-717-230	Sequence 230, App	c 965	11.4	81.4	21513	3	US-09-949-016-16696	Sequence 16696, A
c 893	11.4	81.4	6830	2	US-08-822-445-1	Sequence 1, Appli	c 966	11.4	81.4	21513	3	US-09-949-016-16897	Sequence 16897, A
c 894	11.4	81.4	6830	2	US-09-396-540-1	Sequence 1, Appli	c 967	11.4	81.4	23193	3	US-09-949-016-17215	Sequence 17215, A
c 895	11.4	81.4	6975	3	US-09-949-016-15155	Sequence 15155, A	c 968	11.4	81.4	23568	3	US-09-949-016-14160	Sequence 14160, A
c 896	11.4	81.4	6995	3	US-09-531-266-1	Sequence 1, Appli	c 969	11.4	81.4	23672	3	US-09-949-016-15296	Sequence 15296, A
c 897	11.4	81.4	7070	3	US-09-949-016-12469	Sequence 12469, A	c 970	11.4	81.4	23672	3	US-09-949-016-12575	Sequence 12575, A
c 898	11.4	81.4	7070	3	US-09-949-016-15322	Sequence 15322, A	c 971	11.4	81.4	23672	3	US-09-949-016-14941	Sequence 14941, A
c 899	11.4	81.4	7194	3	US-09-601-326-76	Sequence 76, Appl	c 972	11.4	81.4	24405	3	US-09-949-016-12040	Sequence 12040, A

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989 11.4 81.4 31545 3 US-09-949-016-17219
990 11.4 81.4 32669 3 US-09-949-016-17250
c 991 11.4 81.4 33248 3 US-09-596-002-24
992 11.4 81.4 34446 3 US-09-103-330-35
993 11.4 81.4 34446 3 US-09-871-212-1
994 11.4 81.4 34531 3 US-09-949-016-14604
c 995 11.4 81.4 35081 2 US-08-752-760A-1
c 996 11.4 81.4 35100 3 US-09-782-378A-26
997 11.4 81.4 35337 3 US-09-949-016-17249
c 998 11.4 81.4 35524 3 US-08-923-137-1
c 999 11.4 81.4 36519 3 US-08-923-137-2
c1000 11.4 81.4 37319 3 US-09-949-016-13164

ALIGNMENTS

RESULT 1
US-09-248-796A-1942/c
; Sequence 1942, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1942
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1942

Query Match 100.0%; Score 14; DB 3; Length 774;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGCTTAC 14
|||
Db 761 GAAGGTGCTTAC 748

RESULT 2
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.

; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743.637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169
Query Match 100.0%; Score 14; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAGGTGCTTAC 14
|||
Db 1094 GAAGGTGCTTAC 1081
RESULT 3
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 4
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 14; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1115 GAAGGTGTGCTTAC 1102

RESULT 5
US-09-620-412C-336/c
; Sequence 336, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 6
US-09-598-419-336/c
; Sequence 336, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-598-419-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 7
US-08-309-341-1/c
; Sequence 1, Application US/08309341
; Patent No. 5594119
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5594119o No. 5594119disk of No. 5594119th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 4
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 14; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 1115 GAAGGTGTGCTTAC 1102

RESULT 5
US-09-620-412C-336/c
; Sequence 336, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-620-412C-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 6
US-09-598-419-336/c
; Sequence 336, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSEQ for Windows Version 3.0/4.0
; SEQ ID NO 336
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Chlymadia trachomatis
US-09-598-419-336

Query Match 92.9%; Score 13; DB 3; Length 1758;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 1451 GAAGGTGTGCTTA 1439

RESULT 7
US-08-309-341-1/c
; Sequence 1, Application US/08309341
; Patent No. 5594119
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; APPLICANT: Thompson, Sheryl Ann
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5594119o No. 5594119disk of No. 5594119th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
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;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/309,341
;/ FILING DATE: 16-SEP-1994
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Lowney, Karen A.
;/ REGISTRATION NUMBER: 31,274
;/ REFERENCE/DOCKET NUMBER: 4247.000-US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212 867 0123
;/ TELEFAX: 212 867 0298
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 2068 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: Genomic DNA
;/ ORIGINAL SOURCE:
;/ ORGANISM: Aspergillus niger
;/ FEATURE:
;/ NAME/KEY: intron
;/ LOCATION: 572..632
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: Join (571..633)
;/ US-08-309-341-1
;/
;/ Query Match 92.9%; Score 13; DB 2; Length 2068;
;/ Best Local Similarity 100.0%; Pred. No. 4e+02;
;/ Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;/
;/ QY 2 AAGGTGCTTAC 14
;/ |||||
;/ DB 583 AAGGTGCTTAC 571
;/
;/ RESULT 8
;/ US-08-608-267-1/c
;/ Sequence 1, Application US/08608267
;/ Patent No. 5686663
;/ GENERAL INFORMATION:
;/ APPLICANT: Yaver, Debbie Sue
;/ APPLICANT: Thompson, Sheryl Ann
;/ TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
;/ NUMBER OF SEQUENCES: 4
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: No. 5686663o No. 5686663disk of No. 5686663th America, Inc.
;/ STREET: 405 Lexington Avenue, Suite 6400
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10174-6401
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/608,267
;/ FILING DATE: 28-FEB-1996
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/309,341
;/ FILING DATE: 20-SEP-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Lowney, Karen A.
;/ REGISTRATION NUMBER: 31,274
;/ REFERENCE/DOCKET NUMBER: 4247.000-US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212 867 0123
;/ TELEFAX: 212 867 0298
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 2068 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: Genomic DNA
;/ ORIGINAL SOURCE:
;/ ORGANISM: Aspergillus niger
;/ FEATURE:
;/ NAME/KEY: intron
;/ LOCATION: 572..632
;/ TELEFAX: 212 867 0298
;/ INFORMATION FOR SEQ ID NO: 1:
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;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 2068 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: Genomic DNA
;/ ORIGINAL SOURCE:
;/ ORGANISM: Aspergillus niger
;/ FEATURE:
;/ NAME/KEY: intron
;/ LOCATION: 572..632
;/ FEATURE:
;/ NAME/KEY: CDS
;/ LOCATION: Join (571..633)
;/ US-08-608-267-1
;/
;/ Query Match 92.9%; Score 13; DB 2; Length 2068;
;/ Best Local Similarity 100.0%; Pred. No. 4e+02;
;/ Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;/
;/ QY 2 AAGGTGCTTAC 14
;/ |||||
;/ DB 583 AAGGTGCTTAC 571
;/
;/ RESULT 9
;/ US-08-608-452-1/c
;/ Sequence 1, Application US/08608452
;/ Patent No. 5693510
;/ GENERAL INFORMATION:
;/ APPLICANT: Yaver, Debbie Sue
;/ APPLICANT: Thompson, Sheryl Ann
;/ TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
;/ NUMBER OF SEQUENCES: 4
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: No. 5693510o No. 5693510disk of No. 5693510th America, Inc.
;/ STREET: 405 Lexington Avenue, Suite 6400
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10174-6401
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/608,452
;/ FILING DATE: 28-FEB-1996
;/ CLASSIFICATION: 536
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/309,341
;/ FILING DATE: 20-SEP-1994
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Lowney, Karen A.
;/ REGISTRATION NUMBER: 31,274
;/ REFERENCE/DOCKET NUMBER: 4247.000-US
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 212 867 0123
;/ TELEFAX: 212 867 0298
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 2068 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: Genomic DNA
;/ ORIGINAL SOURCE:
;/ ORGANISM: Aspergillus niger
;/ FEATURE:
;/ NAME/KEY: intron
;/ LOCATION: 572..632
;/ TELEFAX: 212 867 0298
;/ INFORMATION FOR SEQ ID NO: 1:
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; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-608-452-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       583 AAGGTGTGCTTAC 571

RESULT 10
US-08-608-224-1/c
; Sequence 1, Application US/08608224
; Patent No. 5705376
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5705376 No. 5705376disk of No. 5705376th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/608,224
; FILING DATE: 28-FEB-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-608-224-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       583 AAGGTGTGCTTAC 571

RESULT 11
US-08-967-149-1/c
; Sequence 1, Application US/08967149
; Patent No. 5939305
; GENERAL INFORMATION:
; APPLICANT: Yaver, Debbie Sue
; TITLE OF INVENTION: GENE ENCODING CARBOXYPEPTIDASE OF ASPERGILLUS NIGER
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939305 No. 5939305disk of No. 5939305th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,149
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/608,452
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 08/309,341
; FILING DATE: 20-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney, Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4247.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: intron
; LOCATION: 572..632
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join (571..633)
US-08-967-149-1

Query Match          92.9%; Score 13; DB 2; Length 2068;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       583 AAGGTGTGCTTAC 571

RESULT 12
US-10-197-220-165/c
; Sequence 165, Application US/10197220
; Patent No. 6919187
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Guderian, Jeff
; APPLICANT: Skeiky, Yasir A. W.

```

; APPLICANT: Maisonneuve, Jean-Francois L.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
; FILE REFERENCE: 210121.515C3
; CURRENT APPLICATION NUMBER: US/10/197,220
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 175
; SEQ ID NO 165
; LENGTH: 4191
; TYPE: DNA
; ORGANISM: Chlamydia
US-10-197-220-165

Query Match 92.9%; Score 13; DB 3; Length 4191;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||
Db 1925 GAAGGTGTGCTTA 1913

RESULT 13
US-09-556-877-174/c
; Sequence 174, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probat, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Maisonneuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556,877
; CURRENT FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-174

Query Match 92.9%; Score 13; DB 3; Length 5265;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||
Db 2003 GAAGGTGTGCTTA 1991

RESULT 14
US-09-620-412C-174/c
; Sequence 174, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-174

Query Match 92.9%; Score 13; DB 3; Length 5265;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||
Db 2003 GAAGGTGTGCTTA 1991

RESULT 15
US-09-598-419-174/c
; Sequence 174, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598,419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 174
; LENGTH: 5265
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-174

Query Match 92.9%; Score 13; DB 3; Length 5265;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
|||||
Db 2003 GAAGGTGTGCTTA 1991

RESULT 16
US-08-961-527-104/c
; Sequence 104, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 104:

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6735 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-104

Query Match          92.9%; Score 13; DB 3; Length 6735;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       5983 AAGGTGTGCTTAC 5971

RESULT 17
US-09-949-016-11759/c
; Sequence 11759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11759
; LENGTH: 15164
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11759

Query Match          92.9%; Score 13; DB 3; Length 15164;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       13446 AAGGTGTGCTTAC 13434

RESULT 18
US-09-949-016-15664/c
; Sequence 15664, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15664
; LENGTH: 15165
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15664

Query Match          92.9%; Score 13; DB 3; Length 15165;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       13446 AAGGTGTGCTTAC 13434

RESULT 19
US-09-949-016-13632
; Sequence 13632, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13632
; LENGTH: 300402
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(300402)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13632

Query Match          92.9%; Score 13; DB 3; Length 300402;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
        |||||
Db       108237 AAGGTGTGCTTAC 108249

RESULT 20
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
```

```

; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match          92.9%; Score 13; DB 3; Length 767677;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
   |||||
Db 531167 GAAGGTGTGCTTA 531155

RESULT 21
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match          92.9%; Score 13; DB 3; Length 767677;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
   |||||
Db 531167 GAAGGTGTGCTTA 531155

RESULT 22
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(4403765)
; OTHER INFORMATION: n = A,T,C or G
US-09-103-840A-2
```

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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          92.9%; Score 13; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
   |||||
Db 2752175 GAAGGTGTGCTTA 2752187

RESULT 23
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          92.9%; Score 13; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
   |||||
Db 2755365 GAAGGTGTGCTTA 2755377

RESULT 24
US-09-198-452A-1978
; Sequence 1978, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment
; thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1978
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1978

Query Match          88.6%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
   |||||
Db 1 GAAGGTGTCTTAC 14
```

```
RESULT 25
US-09-198-452A-4479/c
; Sequence 4479, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffaia, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4479
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-4479

Query Match      88.6%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
DB      18 GAAGGTGCTTAC 5

RESULT 26
US-10-131-827-258/c
; Sequence 258, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-258

Query Match      88.6%; Score 12.4; DB 3; Length 50;
Best Local Similarity 92.9%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
DB      19 GAAGGTGCTTAC 6

RESULT 27
US-10-131-831-258/c
; Sequence 258, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
```

```
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 258
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-258

Query Match      88.6%; Score 12.4; DB 5; Length 50;
Best Local Similarity 92.9%; Pred. No. 5.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
DB      19 GAAGGTGCTTAC 6

RESULT 28
US-09-583-110-1470
; Sequence 1470, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1470
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1470

Query Match      88.6%; Score 12.4; DB 3; Length 399;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGCTTAC 14
DB      328 GAAGGTGCTTAC 341

RESULT 29
US-09-605-703B-1409/c
; Sequence 1409, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
```

```
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1409
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(385)
; OTHER INFORMATION: RXN03032
US-09-605-703B-1409

Query Match      88.6%; Score 12.4; DB 4; Length 408;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      82 GATGGTGTGCTTAC 69

RESULT 30
US-09-605-703B-1413/c
; Sequence 1413, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1413
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(385)
; OTHER INFORMATION: FRXA00063
US-09-605-703B-1413

Query Match      88.6%; Score 12.4; DB 4; Length 408;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      82 GATGGTGTGCTTAC 69

RESULT 31
US-09-107-433-1001
; Sequence 1001, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
; THERAPEUTICS
```

```
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1001:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...414
; SEQUENCE DESCRIPTION: SEQ ID NO: 1001:
US-09-107-433-1001

Query Match      88.6%; Score 12.4; DB 3; Length 414;
Best Local Similarity 92.9%; Pred. No. 7.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      343 GAAGGTTTGCTTAC 356

RESULT 32
US-09-270-767-7793/c
; Sequence 7793, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7793
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7793

Query Match      88.6%; Score 12.4; DB 3; Length 489;
```

```
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 306 GATGGTGTGCTTAC 293

RESULT 33
US-09-270-767-23075/c
; Sequence 23075, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23075
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23075

Query Match 88.6%; Score 12.4; DB 3; Length 489;
Best Local Similarity 92.9%; Pred. No. 7.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 306 GATGGTGTGCTTAC 293

RESULT 34
US-09-949-016-26439/c
; Sequence 26439, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26439
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-26439

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 126 GAAGGTGTGCTTAC 113

RESULT 35
US-09-949-016-29854
; Sequence 29854, Application US/09949016
; Patent No. 6812339
```

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29854
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-29854

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 454 GAAGGTGTGCTTAC 467

RESULT 36
US-09-949-016-29855
; Sequence 29855, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29855
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-29855

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 32 GAAGGTGTGCTTAC 45

RESULT 37
US-09-949-016-52622/c
; Sequence 52622, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52622
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-52622
```

```
Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GAAGGTGTGCTTAC 14
        |||||
Db      379 GAAGCTGTGCTTAC 366
```

```
RESULT 38
US-09-949-016-55152
; Sequence 55152, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55152
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-55152
```

```
Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GAAGGTGTGCTTAC 14
        |||||
Db      454 GAAGGTGTGCTTAC 467
```

```
RESULT 39
US-09-949-016-55153
; Sequence 55153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
```

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55153
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-55153
```

```
Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GAAGGTGTGCTTAC 14
        |||||
Db      32 GAAGGTGTGCTTAC 45
```

```
RESULT 40
US-09-949-016-58296
; Sequence 58296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58296
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-58296
```

```
Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 GAAGGTGTGCTTAC 14
        |||||
Db      437 GAAGGTGTGCTTAC 450
```

```
RESULT 41
US-09-949-016-66349/c
; Sequence 66349, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
```



```
; SEQ ID NO 66349
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-66349

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 59 GAAGGTGTGCTAC 46

RESULT 42
US-09-949-016-94388/c
; Sequence 94388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94388
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94388

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 126 GAAGGTGTGCTTC 113

RESULT 43
US-09-949-016-105464
; Sequence 105464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105464
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105464

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 232 GAAGGTGTCTTAC 245

RESULT 44
US-09-949-016-105465
; Sequence 105465, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105465
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105465

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14
Db 232 GAAGGTGTCTTAC 245

RESULT 45
US-09-949-016-105466
; Sequence 105466, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105466
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105466

Query Match      88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 GAAGGTGTGCTTAC 14
| | | | | | | | | |
Db 204 GAAGGTGTGCTTAC 217

RESULT 46

US-09-949-016-188180
; Sequence 188180, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188180
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-188180

Query Match 88.6%; Score 12.4; DB 3; Length 601;
Best Local Similarity 92.9%; Pred. No. 7.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
| | | | | | | | | |
Db 470 GAAGGTGTGCTTAC 483

RESULT 47

US-09-533-559-4801/c
; Sequence 4801, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4801
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(649)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-4801

Query Match 88.6%; Score 12.4; DB 3; Length 649;
Best Local Similarity 92.9%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
| | | | | | | | | |
Db 155 GAAGGTGTGCTTAC 142

RESULT 48

US-09-533-559-5196
; Sequence 5196, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5196
; LENGTH: 676
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(676)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-5196

Query Match 88.6%; Score 12.4; DB 3; Length 676;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
| | | | | | | | | |
Db 532 GTAGGTGTGCTTAC 545

RESULT 49

US-09-605-703B-1411/c
; Sequence 1411, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habernauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 1411
; LENGTH: 683
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(660)
; OTHER INFORMATION: RXN03034
US-09-605-703B-1411

Query Match 88.6%; Score 12.4; DB 4; Length 683;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Search completed: May 31, 2006, 21:24:25
Job time : 138 secs

QY 1 GAAGGTGTCCTTAC 14
Db 357 GATGGTGTGCTTAC 344

RESULT 50
US-09-297-648-2528/c
; Sequence 2528, Application US/09297648
; Patent No. 6964868
; GENERAL INFORMATION:
; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominquez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.
; APPLICANT: Pot, David
; APPLICANT: Kassan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
; APPLICANT: Dickson, Mark
; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, William Lee
; APPLICANT: Stache-Crain, Birjit
; TITLE OF INVENTION: No. 6964868el Human Genes and Gene Expression
; FILE REFERENCE: 2300-1481
; CURRENT APPLICATION NUMBER: US/09/297,648
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,666
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,515
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 5252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2528
; LENGTH: 734
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(734)
; OTHER INFORMATION: n = A,T,C or G
US-09-297-648-2528

Query Match 88.6%; Score 12.4; DB 4; Length 734;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTCCTTAC 14
Db 709 GAAGGTGTCCTTAC 696

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:37:46 ; Search time 1470 Seconds
(without alignments)
117.025 Million cell updates/sec

Title: US-09-865-579A-19

Perfect score: 14

Sequence: 1 gaaggtgtcttac 14

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	14	3	US-09-865-579A-17
2	14	100.0	14	3	US-09-865-579A-19
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4	14	100.0	22	10	US-10-735-357-75
C 5	14	100.0	22	10	US-10-995-051-16
6	14	100.0	281	10	US-10-995-051-14
C 7	14	100.0	560	10	US-10-478-633A-151
8	14	100.0	738	6	US-10-027-632-152712
9	14	100.0	738	6	US-10-027-632-152713
10	14	100.0	738	7	US-10-027-632-152712
11	14	100.0	738	7	US-10-027-632-152713
C 12	14	100.0	1502	8	US-10-425-114-2665
C 13	14	100.0	1502	9	US-10-425-115-102549
C 14	14	100.0	1957	9	US-10-479-674-82
C 15	14	100.0	2007	3	US-09-452-599-169
C 16	14	100.0	2007	7	US-10-121-120-169
C 17	14	100.0	2007	9	US-10-479-674-78
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14	100.0	2007	9	US-10-479-674-91	Sequence 91, Appl
14	100.0	2007	9	US-10-121-120-169	Sequence 169, Appl
14	100.0	2015	8	US-10-320-797-1231	Sequence 1231, Ap
14	100.0	2028	8	US-10-724-972A-3141	Sequence 3141, Ap
14	100.0	4015	8	US-10-320-797-231	Sequence 231, App
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13	92.9	201	8	US-10-741-601-18514	Sequence 18514, A
13	92.9	201	9	US-10-741-600-50241	Sequence 50241, A
13	92.9	301	10	US-10-450-763-29551	Sequence 29551, A
13	92.9	335	8	US-10-424-599-6873	Sequence 6873, Ap
13	92.9	339	3	US-09-732-627A-1859	Sequence 1859, Ap
13	92.9	346	8	US-10-424-599-129096	Sequence 129096,
13	92.9	418	4	US-09-925-065A-201193	Sequence 201193,
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	94	13	92.9	570	5	US-09-925-065A-811812	Sequence 811812,	167	13	92.9	1529	8	US-10-425-114-9676	Sequence 9676, Ap
	95	13	92.9	570	5	US-09-925-065A-811812	Sequence 811812,	168	13	92.9	1758	3	US-09-841-132-336	Sequence 336, App
	96	13	92.9	572	6	US-10-027-632-215572	Sequence 215572,	c 169	13	92.9	1758	3	US-10-872-155-336	Sequence 336, App
	97	13	92.9	572	6	US-10-027-632-215573	Sequence 215573,	c 170	13	92.9	1821	8	US-10-705-116A-9	Sequence 9, Appli
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	111	13	92.9	577	5	US-09-925-065A-117032	Sequence 117032,	185	13	92.9	1994	16	US-11-096-568A-34080	Sequence 34080, A
	112	13	92.9	584	12	US-10-301-480-215834	Sequence 215834,	c 186	13	92.9	1999	8	US-10-437-963-16019	Sequence 16019, A
	113	13	92.9	584	12	US-10-301-480-829243	Sequence 829243,	c 187	13	92.9	2063	8	US-10-424-599-1396	Sequence 1396, A
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	163	13	92.9	1242	10	US-10-750-623-30919	Sequence 30919, A	c 237	12.6	90.0	573	5	US-09-925-065A-439653	Sequence 439653,

C 237	12.6	90.0	574	12	US-10-301-480-500710	Sequence 500710,	C 310	12.4	88.6	376	12	US-10-301-480-1073045	Sequence 1073045,
C 238	12.6	90.0	574	12	US-10-301-480-111419	Sequence 114119,	C 311	12.4	88.6	381	3	US-09-732-627A-1613	Sequence 1613, Ap
C 239	12.4	88.6	19	14	US-11-083-784-251000	Sequence 251000,	C 312	12.4	88.6	381	30	US-10-779-543-10524	Sequence 10524, A
C 240	12.4	88.6	19	14	US-11-083-784-465057	Sequence 465057,	C 313	12.4	88.6	386	9	US-10-357-930-46046	Sequence 46046, A
C 241	12.4	88.6	19	14	US-11-083-784-1546339	Sequence 1546339,	C 314	12.4	88.6	386	9	US-10-357-930-47176	Sequence 47176, A
C 242	12.4	88.6	19	15	US-11-101-244-251000	Sequence 251000,	C 315	12.4	88.6	392	9	US-10-425-115-150312	Sequence 150312,
C 243	12.4	88.6	19	15	US-11-101-244-465057	Sequence 465057,	C 316	12.4	88.6	392	9	US-10-425-115-94251	Sequence 94251, A
C 244	12.4	88.6	19	15	US-11-101-244-1546339	Sequence 1546339,	C 317	12.4	88.6	394	10	US-10-779-543-16180	Sequence 16180, A
C 245	12.4	88.6	20	7	US-10-289-762-1978	Sequence 1978, Ap	C 318	12.4	88.6	396	9	US-10-472-928-263	Sequence 263, App
C 246	12.4	88.6	20	7	US-10-289-762-4479	Sequence 4479, Ap	C 319	12.4	88.6	398	9	US-10-425-115-177673	Sequence 177673,
C 247	12.4	88.6	21	11	US-10-310-914A-212681	Sequence 212681,	C 320	12.4	88.6	399	3	US-09-815-243-9114	Sequence 9114, Ap
C 248	12.4	88.6	24	11	US-10-310-914A-212682	Sequence 212682,	C 321	12.4	88.6	399	3	US-09-815-243-9472	Sequence 9472, Ap
C 249	12.4	88.6	25	8	US-10-719-956-50987	Sequence 50987, A	C 322	12.4	88.6	399	8	US-10-282-122A-37553	Sequence 37553, A
C 250	12.4	88.6	25	8	US-10-719-956-256067	Sequence 256067,	C 323	12.4	88.6	403	9	US-10-425-115-169458	Sequence 169458,
C 251	12.4	88.6	25	8	US-10-719-956-311710	Sequence 311710,	C 324	12.4	88.6	404	9	US-10-767-793-1647	Sequence 1647, Ap
C 252	12.4	88.6	25	8	US-10-719-956-389564	Sequence 389564,	C 325	12.4	88.6	408	3	US-09-783-590-3620	Sequence 3620, Ap
C 253	12.4	88.6	25	8	US-10-719-956-450851	Sequence 450851,	C 326	12.4	88.6	414	7	US-10-007-926A-369	Sequence 369, App
C 254	12.4	88.6	25	8	US-10-719-956-573001	Sequence 573001,	C 327	12.4	88.6	414	8	US-10-474-776-445	Sequence 445, App
C 255	12.4	88.6	25	8	US-10-719-956-680581	Sequence 680581,	C 328	12.4	88.6	414	10	US-10-617-320-1001	Sequence 1001, Ap
C 256	12.4	88.6	25	9	US-10-719-900-272853	Sequence 272853,	C 329	12.4	88.6	418	3	US-09-960-352-12566	Sequence 12566, A
C 257	12.4	88.6	25	9	US-10-719-900-431528	Sequence 431528,	C 330	12.4	88.6	433	6	US-10-027-632-183308	Sequence 183308,
C 258	12.4	88.6	25	9	US-10-719-900-440516	Sequence 440516,	C 331	12.4	88.6	433	7	US-10-027-632-183308	Sequence 183308,
C 259	12.4	88.6	25	9	US-10-719-900-644391	Sequence 644391,	C 332	12.4	88.6	436	12	US-10-301-480-272348	Sequence 272348,
C 260	12.4	88.6	25	9	US-10-719-900-898049	Sequence 898049,	C 333	12.4	88.6	436	12	US-10-301-480-885757	Sequence 885757,
C 261	12.4	88.6	25	11	US-10-933-982-81140	Sequence 81140, A	C 334	12.4	88.6	440	4	US-09-925-065A-181686	Sequence 181686,
C 262	12.4	88.6	25	13	US-11-036-317-7709	Sequence 7709, Ap	C 335	12.4	88.6	440	5	US-09-925-065A-181686	Sequence 181686,
C 263	12.4	88.6	25	13	US-11-036-317-8293	Sequence 8293, Ap	C 336	12.4	88.6	442	3	US-09-764-891-658	Sequence 658, App
C 264	12.4	88.6	25	13	US-11-036-317-23791	Sequence 23791, A	C 337	12.4	88.6	459	3	US-09-864-763-102	Sequence 102, App
C 265	12.4	88.6	25	13	US-11-036-317-444094	Sequence 444094,	C 338	12.4	88.6	460	8	US-10-437-963-28842	Sequence 28842, A
C 266	12.4	88.6	25	13	US-11-036-317-634816	Sequence 634816,	C 339	12.4	88.6	466	9	US-10-674-124A-7709	Sequence 7709, Ap
C 267	12.4	88.6	25	15	US-11-121-849-147659	Sequence 147659,	C 340	12.4	88.6	471	4	US-09-925-065A-354629	Sequence 354629,
C 268	12.4	88.6	25	15	US-11-121-849-333005	Sequence 333005,	C 341	12.4	88.6	471	4	US-09-925-065A-354629	Sequence 354629,
C 269	12.4	88.6	25	15	US-11-121-849-469995	Sequence 469995,	C 342	12.4	88.6	471	5	US-09-925-065A-354629	Sequence 354629,
C 270	12.4	88.6	33	9	US-10-784-880-161	Sequence 161, App	C 343	12.4	88.6	471	5	US-09-925-065A-354629	Sequence 354629,
C 271	12.4	88.6	50	7	US-10-131-827-258	Sequence 258, App	C 344	12.4	88.6	474	8	US-10-437-963-18033	Sequence 18033, A
C 272	12.4	88.6	50	16	US-11-175-859-22523	Sequence 22523, A	C 345	12.4	88.6	481	12	US-10-301-480-426189	Sequence 426189
C 273	12.4	88.6	200	16	US-11-098-686-2600	Sequence 2600, Ap	C 346	12.4	88.6	481	12	US-10-301-480-1039598	Sequence 1039598,
C 274	12.4	88.6	201	8	US-10-437-963-85281	Sequence 85281, A	C 347	12.4	88.6	484	9	US-09-918-995-32155	Sequence 32155, A
C 275	12.4	88.6	201	9	US-10-719-993-28792	Sequence 28792, A	C 348	12.4	88.6	489	3	US-09-918-995-32155	Sequence 32155, A
C 276	12.4	88.6	201	10	US-10-995-561-29917	Sequence 29917, A	C 349	12.4	88.6	490	4	US-09-925-065A-369726	Sequence 369726,
C 277	12.4	88.6	201	10	US-10-995-561-57506	Sequence 57506, A	C 350	12.4	88.6	490	4	US-09-925-065A-369727	Sequence 369727,
C 278	12.4	88.6	201	10	US-10-995-561-57529	Sequence 57529, A	C 351	12.4	88.6	490	4	US-09-925-065A-611327	Sequence 611327,
C 279	12.4	88.6	201	10	US-10-995-561-68777	Sequence 68777, A	C 352	12.4	88.6	490	5	US-09-925-065A-369726	Sequence 369726,
C 280	12.4	88.6	201	15	US-11-124-368A-7150	Sequence 7150, Ap	C 353	12.4	88.6	490	5	US-09-925-065A-369727	Sequence 369727,
C 281	12.4	88.6	201	16	US-11-124-368A-11403	Sequence 11403, A	C 354	12.4	88.6	490	5	US-09-925-065A-611327	Sequence 611327,
C 282	12.4	88.6	201	16	US-11-124-367A-10054	Sequence 10054, A	C 355	12.4	88.6	490	8	US-10-767-701-22110	Sequence 22110, A
C 283	12.4	88.6	201	16	US-11-124-367A-12387	Sequence 12387, A	C 356	12.4	88.6	491	4	US-09-925-065A-844615	Sequence 844615,
C 284	12.4	88.6	201	16	US-11-124-367A-12388	Sequence 12388, A	C 357	12.4	88.6	491	5	US-09-925-065A-844615	Sequence 844615,
C 285	12.4	88.6	201	16	US-11-124-367A-21774	Sequence 21774, A	C 358	12.4	88.6	491	12	US-10-301-480-439811	Sequence 439811,
C 286	12.4	88.6	233	3	US-09-983-963-5426	Sequence 5426, Ap	C 359	12.4	88.6	491	12	US-10-301-480-439812	Sequence 439812,
C 287	12.4	88.6	233	9	US-10-357-930-16429	Sequence 16429, A	C 360	12.4	88.6	491	12	US-10-301-480-1053220	Sequence 1053220,
C 288	12.4	88.6	241	12	US-10-301-480-398388	Sequence 398388,	C 361	12.4	88.6	491	12	US-10-301-480-1053221	Sequence 1053221,
C 289	12.4	88.6	241	12	US-10-301-480-1011797	Sequence 1011797,	C 362	12.4	88.6	492	9	US-10-425-115-1411	Sequence 1411, Ap
C 290	12.4	88.6	244	4	US-09-925-065A-323943	Sequence 323943,	C 363	12.4	88.6	493	4	US-09-925-065A-539179	Sequence 539179,
C 291	12.4	88.6	244	5	US-09-925-065A-323943	Sequence 323943,	C 364	12.4	88.6	493	4	US-09-925-065A-539180	Sequence 539180,
C 292	12.4	88.6	254	8	US-10-424-599-109218	Sequence 109218,	C 365	12.4	88.6	493	5	US-09-925-065A-539179	Sequence 539179,
C 293	12.4	88.6	275	9	US-10-357-930-16220	Sequence 16220, A	C 366	12.4	88.6	493	5	US-09-925-065A-539180	Sequence 539180,
C 294	12.4	88.6	282	9	US-10-357-930-17353	Sequence 17353, A	C 367	12.4	88.6	493	8	US-10-424-599-82326	Sequence 82326, A
C 295	12.4	88.6	313	3	US-09-764-891-7077	Sequence 7077, Ap	C 368	12.4	88.6	495	3	US-09-918-995-30723	Sequence 30723, A
C 296	12.4	88.6	320	7	US-10-007-926A-279	Sequence 279, App	C 369	12.4	88.6	496	4	US-09-925-065A-532142	Sequence 532142,
C 297	12.4	88.6	321	9	US-10-425-115-17912	Sequence 17912,	C 370	12.4	88.6	496	4	US-09-925-065A-532143	Sequence 532143,
C 298	12.4	88.6	329	9	US-10-357-930-46255	Sequence 46255, A	C 371	12.4	88.6	496	5	US-09-925-065A-532142	Sequence 532142,
C 299	12.4	88.6	333	7	US-10-369-493-45351	Sequence 45351, A	C 372	12.4	88.6	496	5	US-09-925-065A-532143	Sequence 532143,
C 300	12.4	88.6	350	8	US-10-424-599-86263	Sequence 86263, A	C 373	12.4	88.6	497	9	US-10-425-115-181434	Sequence 181434,
C 301	12.4	88.6	353	7	US-10-029-386-17106	Sequence 17106, A	C 374	12.4	88.6	500	3	US-09-783-590-3621	Sequence 3621, Ap
C 302	12.4	88.6	357	4	US-09-925-065A-391409	Sequence 391409,	C 375	12.4	88.6	501	4	US-09-925-065A-164891	Sequence 164891,
C 303	12.4	88.6	357	5	US-09-925-065A-391409	Sequence 391409,	C 376	12.4	88.6	501	5	US-09-925-065A-164891	Sequence 164891,
C 304	12.4	88.6	364	8	US-10-437-963-90151	Sequence 90151, A	C 377	12.4	88.6	506	12	US-10-301-480-386350	Sequence 386350,
C 305	12.4	88.6	371	4	US-09-925-065A-616000	Sequence 616000,	C 378	12.4	88.6	506	12	US-10-301-480-999759	Sequence 999759,
C 306	12.4	88.6	371	5	US-09-925-065A-616000	Sequence 616000,	C 379	12.4	88.6	507	4	US-09-925-065A-310923	Sequence 310923,
C 307	12.4	88.6	372	3	US-10-156-761-1243	Sequence 1243, Ap	C 380	12.4	88.6	507	5	US-09-925-065A-310923	Sequence 310923,
C 308	12.4	88.6	376	3	US-09-918-995-4426	Sequence 4426, Ap	C 381	12.4	88.6	507	10	US-10-779-543-16141	Sequence 16141, A
C 309	12.4	88.6	376	12	US-10-301-480-459636	Sequence 459636,	C 382	12.4	88.6	508	12	US-10-301-480-457226	Sequence 457226,

C 383	12.4	88.6	508	12	US-10-301-480-870635	Sequence 870635,	456	12.4	88.6	554	12	US-10-301-480-468168	Sequence 468168,
C 384	12.4	88.6	510	4	US-09-925-065A-164892	Sequence 164892,	457	12.4	88.6	554	12	US-10-301-480-1081577	Sequence 1081577,
C 385	12.4	88.6	510	5	US-09-925-065A-164892	Sequence 164892,	458	12.4	88.6	555	4	US-09-925-065A-798660	Sequence 798660,
C 386	12.4	88.6	510	16	US-11-079-463-3936	Sequence 3936, Ap	459	12.4	88.6	555	4	US-09-925-065A-945710	Sequence 945710,
C 387	12.4	88.6	515	9	US-10-425-115-152409	Sequence 152409,	460	12.4	88.6	555	5	US-09-925-065A-798660	Sequence 798660,
C 388	12.4	88.6	517	12	US-10-301-480-9	Sequence 9, Appli	461	12.4	88.6	555	5	US-09-925-065A-945710	Sequence 945710,
C 389	12.4	88.6	517	12	US-10-301-480-257227	Sequence 257227,	c 462	12.4	88.6	556	4	US-09-925-065A-18150	Sequence 18150, A
C 390	12.4	88.6	517	12	US-10-301-480-613418	Sequence 613418,	c 463	12.4	88.6	556	5	US-09-925-065A-18150	Sequence 18150, A
C 391	12.4	88.6	517	12	US-10-301-480-870636	Sequence 870636,	c 464	12.4	88.6	556	12	US-10-301-480-119387	Sequence 119387,
C 392	12.4	88.6	518	6	US-10-027-632-98340	Sequence 98340, A	c 465	12.4	88.6	556	12	US-10-301-480-732796	Sequence 732796,
C 393	12.4	88.6	518	7	US-10-027-632-98340	Sequence 98340, A	c 466	12.4	88.6	557	4	US-09-925-065A-435867	Sequence 435867,
C 394	12.4	88.6	521	6	US-10-198-846-8321	Sequence 8321, Ap	467	12.4	88.6	557	4	US-09-925-065A-435868	Sequence 435868,
C 395	12.4	88.6	521	7	US-10-029-386-4001	Sequence 4001, Ap	468	12.4	88.6	557	4	US-09-925-065A-435869	Sequence 435869,
C 396	12.4	88.6	524	9	US-10-425-115-7448	Sequence 7448, Ap	469	12.4	88.6	557	5	US-09-925-065A-435867	Sequence 435867,
C 397	12.4	88.6	526	4	US-09-925-065A-332775	Sequence 332775,	470	12.4	88.6	557	5	US-09-925-065A-435868	Sequence 435868,
C 398	12.4	88.6	526	5	US-09-925-065A-332775	Sequence 332775,	471	12.4	88.6	557	5	US-09-925-065A-435869	Sequence 435869,
C 399	12.4	88.6	528	4	US-09-925-065A-15310	Sequence 15310, A	c 472	12.4	88.6	558	4	US-09-925-065A-615757	Sequence 615757,
C 400	12.4	88.6	528	4	US-09-925-065A-15311	Sequence 15311, A	c 473	12.4	88.6	558	5	US-09-925-065A-615757	Sequence 615757,
C 401	12.4	88.6	528	5	US-09-925-065A-15310	Sequence 15310, A	c 474	12.4	88.6	561	7	US-10-029-386-3404	Sequence 3404, Ap
C 402	12.4	88.6	528	5	US-09-925-065A-15311	Sequence 15311, A	c 475	12.4	88.6	562	4	US-09-925-065A-583934	Sequence 583934,
C 403	12.4	88.6	528	12	US-10-301-480-116547	Sequence 116547,	c 476	12.4	88.6	562	5	US-09-925-065A-583934	Sequence 583934,
C 404	12.4	88.6	528	12	US-10-301-480-116548	Sequence 116548,	c 477	12.4	88.6	564	4	US-09-925-065A-793338	Sequence 793338,
C 405	12.4	88.6	528	12	US-10-301-480-729956	Sequence 729956,	c 478	12.4	88.6	564	4	US-09-925-065A-793339	Sequence 793339,
C 406	12.4	88.6	528	12	US-10-301-480-729957	Sequence 729957,	c 479	12.4	88.6	564	4	US-09-925-065A-849688	Sequence 849688,
C 407	12.4	88.6	529	4	US-09-925-065A-563678	Sequence 563678,	c 480	12.4	88.6	564	4	US-09-925-065A-849689	Sequence 849689,
C 408	12.4	88.6	529	4	US-09-925-065A-563679	Sequence 563679,	c 481	12.4	88.6	564	5	US-09-925-065A-793338	Sequence 793338,
C 409	12.4	88.6	529	5	US-09-925-065A-563678	Sequence 563678,	c 482	12.4	88.6	564	5	US-09-925-065A-793339	Sequence 793339,
C 410	12.4	88.6	529	5	US-09-925-065A-563679	Sequence 563679,	c 483	12.4	88.6	564	5	US-09-925-065A-849688	Sequence 849688,
C 411	12.4	88.6	530	6	US-10-027-632-51449	Sequence 51449, A	c 484	12.4	88.6	566	4	US-09-925-065A-534050	Sequence 534050,
C 412	12.4	88.6	530	6	US-10-027-632-51449	Sequence 51449, A	c 485	12.4	88.6	566	4	US-09-925-065A-534050	Sequence 534050,
C 413	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 486	12.4	88.6	567	4	US-09-925-065A-349379	Sequence 349379,
C 414	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 487	12.4	88.6	567	4	US-09-925-065A-349379	Sequence 349379,
C 415	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 488	12.4	88.6	567	5	US-09-925-065A-349379	Sequence 349379,
C 416	12.4	88.6	530	7	US-10-027-632-321291	Sequence 321291,	c 489	12.4	88.6	569	4	US-09-925-065A-339327	Sequence 339327,
C 417	12.4	88.6	530	9	US-10-425-115-62072	Sequence 62072, A	c 490	12.4	88.6	569	5	US-09-925-065A-339327	Sequence 339327,
C 418	12.4	88.6	534	12	US-10-301-480-406421	Sequence 406421,	c 491	12.4	88.6	571	4	US-09-925-065A-401004	Sequence 401004,
C 419	12.4	88.6	534	12	US-10-301-480-1019830	Sequence 1019830,	c 492	12.4	88.6	571	4	US-09-925-065A-443186	Sequence 443186,
C 420	12.4	88.6	535	7	US-10-029-386-1254	Sequence 1254, Ap	c 493	12.4	88.6	571	5	US-09-925-065A-401004	Sequence 401004,
C 421	12.4	88.6	538	4	US-09-925-065A-188125	Sequence 188125,	c 494	12.4	88.6	571	5	US-09-925-065A-443186	Sequence 443186,
C 422	12.4	88.6	538	5	US-09-925-065A-188125	Sequence 188125,	c 495	12.4	88.6	572	6	US-10-027-632-184982	Sequence 184982,
C 423	12.4	88.6	539	4	US-09-925-065A-46112	Sequence 46112, A	c 496	12.4	88.6	572	6	US-10-027-632-184982	Sequence 184982,
C 424	12.4	88.6	539	4	US-09-925-065A-192185	Sequence 192185,	c 497	12.4	88.6	574	4	US-09-925-065A-343030	Sequence 343030,
C 425	12.4	88.6	539	4	US-09-925-065A-197443	Sequence 197443,	c 498	12.4	88.6	574	4	US-09-925-065A-343030	Sequence 343030,
C 426	12.4	88.6	539	5	US-09-925-065A-46112	Sequence 46112, A	c 499	12.4	88.6	574	5	US-09-925-065A-343030	Sequence 343030,
C 427	12.4	88.6	539	5	US-09-925-065A-192185	Sequence 192185,	c 500	12.4	88.6	574	5	US-09-925-065A-343030	Sequence 343030,
C 428	12.4	88.6	539	5	US-09-925-065A-197443	Sequence 197443,	c 501	12.4	88.6	574	9	US-10-425-115-90364	Sequence 90364, A
C 429	12.4	88.6	539	12	US-10-301-480-147350	Sequence 147350,	c 502	12.4	88.6	576	12	US-10-301-480-214276	Sequence 214276,
C 430	12.4	88.6	539	12	US-10-301-480-760759	Sequence 760759,	c 503	12.4	88.6	576	12	US-10-301-480-827685	Sequence 827685,
C 431	12.4	88.6	542	8	US-10-767-701-25615	Sequence 25615, A	c 504	12.4	88.6	577	4	US-09-925-065A-115297	Sequence 115297,
C 432	12.4	88.6	543	4	US-09-925-065A-770952	Sequence 770952,	c 505	12.4	88.6	577	4	US-09-925-065A-925093	Sequence 925093,
C 433	12.4	88.6	543	5	US-09-925-065A-770952	Sequence 770952,	c 506	12.4	88.6	577	5	US-09-925-065A-115297	Sequence 115297,
C 434	12.4	88.6	543	12	US-10-301-480-286389	Sequence 286389,	c 507	12.4	88.6	577	5	US-09-925-065A-925093	Sequence 925093,
C 435	12.4	88.6	543	12	US-10-301-480-899798	Sequence 899798,	c 508	12.4	88.6	577	5	US-10-027-632-284927	Sequence 284927,
C 436	12.4	88.6	544	12	US-10-301-480-281751	Sequence 281751,	c 509	12.4	88.6	577	7	US-10-027-632-284927	Sequence 284927,
C 437	12.4	88.6	544	12	US-10-301-480-895160	Sequence 895160,	c 510	12.4	88.6	580	12	US-10-301-480-366598	Sequence 366598,
C 438	12.4	88.6	548	4	US-09-925-065A-306500	Sequence 306500,	c 511	12.4	88.6	580	12	US-10-301-480-382404	Sequence 382404,
C 439	12.4	88.6	548	4	US-09-925-065A-306501	Sequence 306501,	c 512	12.4	88.6	580	12	US-10-301-480-382405	Sequence 382405,
C 440	12.4	88.6	548	4	US-09-925-065A-306502	Sequence 306502,	c 513	12.4	88.6	580	12	US-10-301-480-382406	Sequence 382406,
C 441	12.4	88.6	548	4	US-09-925-065A-306503	Sequence 306503,	c 514	12.4	88.6	580	12	US-10-301-480-980007	Sequence 980007,
C 442	12.4	88.6	548	5	US-09-925-065A-306500	Sequence 306500,	c 515	12.4	88.6	580	12	US-10-301-480-995813	Sequence 995813,
C 443	12.4	88.6	548	5	US-09-925-065A-306501	Sequence 306501,	c 516	12.4	88.6	580	12	US-10-301-480-995814	Sequence 995814,
C 444	12.4	88.6	548	5	US-09-925-065A-306502	Sequence 306502,	c 517	12.4	88.6	580	12	US-10-301-480-995815	Sequence 995815,
C 445	12.4	88.6	548	5	US-09-925-065A-306503	Sequence 306503,	c 518	12.4	88.6	581	4	US-09-925-065A-289696	Sequence 289696,
C 446	12.4	88.6	551	4	US-09-925-065A-470875	Sequence 470875,	c 519	12.4	88.6	581	5	US-09-925-065A-289696	Sequence 289696,
C 447	12.4	88.6	551	5	US-09-925-065A-470875	Sequence 470875,	c 520	12.4	88.6	581	12	US-10-301-480-415741	Sequence 415741,
C 448	12.4	88.6	553	4	US-09-925-065A-44794	Sequence 44794, A	c 521	12.4	88.6	581	12	US-10-301-480-415742	Sequence 415742,
C 449	12.4	88.6	553	4	US-09-925-065A-44795	Sequence 44795, A	c 522	12.4	88.6	581	12	US-10-301-480-1029150	Sequence 1029150,
C 450	12.4	88.6	553	5	US-09-925-065A-44794	Sequence 44794, A	c 523	12.4	88.6	581	12	US-10-301-480-1029151	Sequence 1029151,
C 451	12.4	88.6	553	5	US-09-925-065A-44795	Sequence 44795, A	c 524	12.4	88.6	585	4	US-09-925-065A-433545	Sequence 433545,
C 452	12.4	88.6	553	12	US-10-301-480-146032	Sequence 146032,	c 525	12.4	88.6	585	5	US-09-925-065A-433545	Sequence 433545,
C 453	12.4	88.6	553	12	US-10-301-480-146033	Sequence 146033,	c 526	12.4	88.6	585	4	US-09-925-065A-165655	Sequence 165655,
C 454	12.4	88.6	553	12	US-10-301-480-759441	Sequence 759441,	c 527	12.4	88.6	586	4	US-09-925-065A-165656	Sequence 165656,
C 455	12.4	88.6	553	12	US-10-301-480-759442	Sequence 759442,	c 528	12.4	88.6	586	5	US-09-925-065A-165655	Sequence 165655,

c 675	12.4	88.6	716	12	US-10-301-480-531568	Sequence 531568,	c 748	12.4	88.6	995	13	US-11-082-308-4	Sequence 4, Appli
c 676	12.4	88.6	716	12	US-10-301-480-1144977	Sequence 1144977,	c 749	12.4	88.6	995	13	US-11-082-308-12	Sequence 12, Appl
c 677	12.4	88.6	719	6	US-10-027-632-23328	Sequence 23328, A	c 750	12.4	88.6	1000	8	US-10-424-539-100700	Sequence 100700,
c 678	12.4	88.6	719	7	US-10-027-632-23328	Sequence 23328, A	c 751	12.4	88.6	1008	8	US-10-432-737-4	Sequence 4, Appli
c 679	12.4	88.6	734	10	US-10-779-543-3372	Sequence 3372, Ap	c 752	12.4	88.6	1008	13	US-11-097-143-19418	Sequence 19418, A
c 680	12.4	88.6	738	6	US-10-027-632-11788	Sequence 11788, A	c 753	12.4	88.6	1014	16	US-11-172-740-213	Sequence 213, App
c 681	12.4	88.6	738	7	US-10-027-632-11788	Sequence 11788, A	c 754	12.4	88.6	1019	16	US-11-096-568A-2921	Sequence 2921, Ap
c 682	12.4	88.6	743	4	US-09-925-065A-8161	Sequence 8161, Ap	c 755	12.4	88.6	1045	10	US-10-750-185-27306	Sequence 27306, A
c 683	12.4	88.6	743	5	US-09-925-065A-8161	Sequence 8161, Ap	c 756	12.4	88.6	1045	10	US-10-750-623-27306	Sequence 27306, A
c 684	12.4	88.6	743	12	US-10-301-480-109398	Sequence 109398,	c 757	12.4	88.6	1134	4	US-09-925-065A-705395	Sequence 705395,
c 685	12.4	88.6	743	12	US-10-301-480-722807	Sequence 722807,	c 758	12.4	88.6	1134	4	US-09-925-065A-705395	Sequence 705395,
c 686	12.4	88.6	744	4	US-09-925-065A-33509	Sequence 33509, A	c 759	12.4	88.6	1134	4	US-09-925-065A-705395	Sequence 705395,
c 687	12.4	88.6	744	4	US-09-925-065A-33510	Sequence 33510, A	c 760	12.4	88.6	1160	4	US-09-925-065A-707076	Sequence 707076,
c 688	12.4	88.6	744	5	US-09-925-065A-33510	Sequence 33509, A	c 761	12.4	88.6	1160	4	US-09-925-065A-707076	Sequence 707076,
c 689	12.4	88.6	744	5	US-09-925-065A-33510	Sequence 33510, A	c 762	12.4	88.6	1161	11	US-10-932-182A-3002	Sequence 3002, Ap
c 690	12.4	88.6	744	12	US-10-301-480-134747	Sequence 134747,	c 763	12.4	88.6	1162	4	US-09-925-065A-706984	Sequence 706984,
c 691	12.4	88.6	744	12	US-10-301-480-134748	Sequence 134748,	c 764	12.4	88.6	1162	4	US-09-925-065A-706985	Sequence 706985,
c 692	12.4	88.6	744	12	US-10-301-480-748156	Sequence 748156,	c 765	12.4	88.6	1162	5	US-09-925-065A-706984	Sequence 706984,
c 693	12.4	88.6	744	12	US-10-301-480-748157	Sequence 748157,	c 766	12.4	88.6	1162	5	US-09-925-065A-706985	Sequence 706985,
c 694	12.4	88.6	747	4	US-09-925-065A-943903	Sequence 943903,	c 767	12.4	88.6	1173	3	US-09-938-842A-1515	Sequence 1515, Ap
c 695	12.4	88.6	747	5	US-09-925-065A-943903	Sequence 943903,	c 768	12.4	88.6	1173	3	US-09-938-842A-1515	Sequence 1515, Ap
c 696	12.4	88.6	747	12	US-10-301-480-540822	Sequence 540822,	c 769	12.4	88.6	1173	3	US-09-938-842A-1515	Sequence 1515, Ap
c 697	12.4	88.6	747	12	US-10-301-480-1154231	Sequence 1154231,	c 770	12.4	88.6	1187	3	US-09-801-574-47	Sequence 47, Appl
c 698	12.4	88.6	750	4	US-09-925-065A-943675	Sequence 943675,	c 771	12.4	88.6	1188	8	US-10-437-963-77288	Sequence 77288, A
c 699	12.4	88.6	750	5	US-09-925-065A-943675	Sequence 943675,	c 772	12.4	88.6	1190	8	US-10-437-963-77288	Sequence 77288, A
c 700	12.4	88.6	759	3	US-09-974-300-2230	Sequence 2230, Ap	c 773	12.4	88.6	1190	8	US-10-437-963-77288	Sequence 77288, A
c 701	12.4	88.6	762	6	US-10-027-632-149879	Sequence 149879,	c 774	12.4	88.6	1197	10	US-10-954-778-38	Sequence 38, Appl
c 702	12.4	88.6	762	6	US-10-027-632-149880	Sequence 149880,	c 775	12.4	88.6	1203	16	US-11-098-686-9083	Sequence 9083, Ap
c 703	12.4	88.6	762	6	US-10-027-632-149881	Sequence 149880,	c 776	12.4	88.6	1209	8	US-10-424-599-33867	Sequence 33867, A
c 704	12.4	88.6	762	7	US-10-027-632-149879	Sequence 149879,	c 777	12.4	88.6	1226	12	US-10-301-480-34638	Sequence 34638, A
c 705	12.4	88.6	762	7	US-10-027-632-149880	Sequence 149880,	c 778	12.4	88.6	1226	12	US-10-301-480-648047	Sequence 648047,
c 706	12.4	88.6	762	7	US-10-027-632-149880	Sequence 149880,	c 779	12.4	88.6	1246	10	US-10-764-420-2013	Sequence 2013, Ap
c 707	12.4	88.6	763	6	US-10-027-632-27666	Sequence 27666, A	c 780	12.4	88.6	1253	8	US-10-432-737-3	Sequence 3, Appli
c 708	12.4	88.6	763	7	US-10-027-632-27666	Sequence 27666, A	c 781	12.4	88.6	1261	8	US-10-494-010-7	Sequence 7, Appli
c 709	12.4	88.6	765	9	US-10-437-963-69635	Sequence 69635, A	c 782	12.4	88.6	1262	10	US-10-424-599-109203	Sequence 109203,
c 710	12.4	88.6	765	9	US-10-793-639-450	Sequence 450, App	c 783	12.4	88.6	1262	10	US-10-750-185-38610	Sequence 38610, A
c 711	12.4	88.6	765	11	US-10-932-182A-77707	Sequence 77707, A	c 784	12.4	88.6	1277	6	US-10-750-623-38610	Sequence 38610, A
c 712	12.4	88.6	771	10	US-10-750-185-44080	Sequence 44080, A	c 785	12.4	88.6	1277	6	US-10-027-632-124926	Sequence 124926,
c 713	12.4	88.6	771	10	US-10-750-623-44080	Sequence 44080, A	c 786	12.4	88.6	1277	7	US-10-027-632-124926	Sequence 124926,
c 714	12.4	88.6	783	9	US-10-425-115-150360	Sequence 150360,	c 787	12.4	88.6	1315	6	US-10-450-763-25425	Sequence 25425, A
c 715	12.4	88.6	783	9	US-10-425-115-150360	Sequence 150360,	c 788	12.4	88.6	1315	6	US-10-027-632-124206	Sequence 124206,
c 716	12.4	88.6	784	7	US-10-027-632-112871	Sequence 112871,	c 789	12.4	88.6	1315	7	US-10-027-632-124206	Sequence 124206,
c 717	12.4	88.6	784	7	US-10-027-632-112871	Sequence 112871,	c 790	12.4	88.6	1317	8	US-10-282-122A-12541	Sequence 12541, A
c 718	12.4	88.6	807	2	US-08-961-527-357	Sequence 357, App	c 791	12.4	88.6	1318	10	US-10-750-623-25707	Sequence 25707, A
c 719	12.4	88.6	807	3	US-09-738-626-1676	Sequence 1676, Ap	c 792	12.4	88.6	1318	10	US-10-750-623-25707	Sequence 25707, A
c 720	12.4	88.6	807	3	US-09-738-626-1676	Sequence 1676, Ap	c 793	12.4	88.6	1323	3	US-09-815-242-9609	Sequence 9609, Ap
c 721	12.4	88.6	816	7	US-10-158-844-357	Sequence 357, App	c 794	12.4	88.6	1350	4	US-09-925-065A-728412	Sequence 728412,
c 722	12.4	88.6	816	7	US-10-158-844-357	Sequence 357, App	c 795	12.4	88.6	1350	5	US-09-925-065A-728412	Sequence 728412,
c 723	12.4	88.6	825	6	US-10-027-632-131981	Sequence 131981,	c 796	12.4	88.6	1362	16	US-11-079-463-2005	Sequence 2005, Ap
c 724	12.4	88.6	825	6	US-10-027-632-131981	Sequence 131981,	c 797	12.4	88.6	1405	10	US-10-750-185-39644	Sequence 39644, A
c 725	12.4	88.6	825	6	US-10-027-632-131981	Sequence 131981,	c 798	12.4	88.6	1405	10	US-10-750-623-39644	Sequence 39644, A
c 726	12.4	88.6	830	12	US-10-424-599-136528	Sequence 136528,	c 799	12.4	88.6	1412	8	US-10-260-238-747	Sequence 747, App
c 727	12.4	88.6	830	12	US-10-301-480-537820	Sequence 537820,	c 800	12.4	88.6	1415	13	US-11-054-191-5	Sequence 5, Appli
c 728	12.4	88.6	834	12	US-10-301-480-1151229	Sequence 1151229,	c 801	12.4	88.6	1415	3	US-09-891-641-70	Sequence 70, Appl
c 729	12.4	88.6	834	7	US-10-313-542-288	Sequence 288, App	c 802	12.4	88.6	1415	3	US-09-891-641-70	Sequence 9, Appli
c 730	12.4	88.6	846	7	US-10-029-386-24801	Sequence 24801, A	c 803	12.4	88.6	1416	6	US-10-235-939-9	Sequence 9, Appli
c 731	12.4	88.6	855	8	US-10-437-963-58095	Sequence 58095, A	c 804	12.4	88.6	1416	7	US-10-602-747A-70	Sequence 70, Appl
c 732	12.4	88.6	858	8	US-10-437-963-58095	Sequence 58095, A	c 805	12.4	88.6	1416	8	US-10-954-778-176	Sequence 176, App
c 733	12.4	88.6	862	10	US-10-282-122A-41769	Sequence 41769, A	c 806	12.4	88.6	1416	10	US-10-954-778-176	Sequence 176, App
c 734	12.4	88.6	862	10	US-10-989-891-46	Sequence 46, Appl	c 807	12.4	88.6	1416	10	US-10-502-040-3	Sequence 3, Appli
c 735	12.4	88.6	891	5	US-09-925-065A-688800	Sequence 688800,	c 808	12.4	88.6	1416	10	US-10-502-040-20	Sequence 20, Appl
c 736	12.4	88.6	891	5	US-09-925-065A-688800	Sequence 688800,	c 809	12.4	88.6	1418	10	US-10-913-142-1	Sequence 1, Appli
c 737	12.4	88.6	892	8	US-10-398-221-1459	Sequence 1459, Ap	c 810	12.4	88.6	1418	15	US-11-193-981-1	Sequence 1, Appli
c 738	12.4	88.6	900	8	US-10-767-701-12268	Sequence 12268, A	c 811	12.4	88.6	1438	7	US-10-369-493-39173	Sequence 39173, A
c 739	12.4	88.6	904	10	US-10-750-185-26656	Sequence 26656, A	c 812	12.4	88.6	1438	7	US-10-369-493-39544	Sequence 39544, A
c 740	12.4	88.6	912	6	US-10-750-623-26656	Sequence 26656, A	c 813	12.4	88.6	1438	7	US-10-369-493-39919	Sequence 39919, A
c 741	12.4	88.6	912	6	US-10-027-632-137074	Sequence 137074,	c 814	12.4	88.6	1451	3	US-09-880-107-1595	Sequence 1595, Ap
c 742	12.4	88.6	922	8	US-10-027-632-137074	Sequence 137074,	c 815	12.4	88.6	1451	8	US-10-007-926A-281	Sequence 281, App
c 743	12.4	88.6	925	7	US-10-027-632-154674	Sequence 154674,	c 816	12.4	88.6	1451	9	US-10-641-643-1271	Sequence 1271, Ap
c 744	12.4	88.6	940	12	US-10-641-643-667	Sequence 154674,	c 817	12.4	88.6	1451	9	US-10-823-253-57	Sequence 57, Appl
c 745	12.4	88.6	940	12	US-10-301-480-543626	Sequence 543626,	c 818	12.4	88.6	1451	9	US-10-278-698-564	Sequence 564, App
c 746	12.4	88.6	992	12	US-10-301-480-1157035	Sequence 1157035,	c 819	12.4	88.6	1451	10	US-10-823-810-57	Sequence 57, Appl
c 747	12.4	88.6	995	6	US-10-021-509-4	Sequence 4, Appli	c 820	12.4	88.6	1451	10	US-10-287-436A-44	Sequence 44, Appl

C 821	12.4	88.6	1451	10	US-10-287-436A-574	Sequence 574, App	894	12.4	88.6	2192	8	US-10-302-172-658	Sequence 658, App
C 822	12.4	88.6	1451	15	US-11-105-268-57	Sequence 57, App	895	12.4	88.6	2224	6	US-10-027-632-102238	Sequence 102238, App
C 823	12.4	88.6	1456	3	US-09-822-849A-159	Sequence 159, App	896	12.4	88.6	2224	7	US-10-027-632-102238	Sequence 102238, App
C 824	12.4	88.6	1465	4	US-09-925-065A-724783	Sequence 724783, A	C 897	12.4	88.6	2226	8	US-10-437-963-101510	Sequence 101510, A
C 825	12.4	88.6	1465	4	US-09-925-065A-724784	Sequence 724784, A	C 898	12.4	88.6	2231	8	US-10-437-963-101510	Sequence 101510, A
C 826	12.4	88.6	1465	4	US-09-925-065A-724785	Sequence 724785, A	C 899	12.4	88.6	2251	9	US-10-739-930-4634	Sequence 70909, A
C 827	12.4	88.6	1465	4	US-09-925-065A-724786	Sequence 724786, A	C 900	12.4	88.6	2251	9	US-10-739-930-4634	Sequence 70909, A
C 828	12.4	88.6	1465	4	US-09-925-065A-724787	Sequence 724787, A	C 901	12.4	88.6	2259	4	US-09-925-065A-702883	Sequence 702883, A
C 829	12.4	88.6	1465	5	US-09-925-065A-724783	Sequence 724783, A	C 902	12.4	88.6	2259	4	US-09-925-065A-702884	Sequence 702884, A
C 830	12.4	88.6	1465	5	US-09-925-065A-724784	Sequence 724784, A	C 903	12.4	88.6	2259	5	US-09-925-065A-702884	Sequence 702884, A
C 831	12.4	88.6	1465	5	US-09-925-065A-724785	Sequence 724785, A	C 904	12.4	88.6	2279	6	US-10-425-115-43622	Sequence 43622, A
C 832	12.4	88.6	1465	5	US-09-925-065A-724786	Sequence 724786, A	C 905	12.4	88.6	2324	6	US-10-027-632-265879	Sequence 265879, A
C 833	12.4	88.6	1465	5	US-09-925-065A-724787	Sequence 724787, A	C 906	12.4	88.6	2324	7	US-10-027-632-265879	Sequence 265879, A
C 834	12.4	88.6	1473	3	US-09-738-626-1401	Sequence 1401, App	C 907	12.4	88.6	2324	12	US-10-301-480-100707	Sequence 100707, A
C 835	12.4	88.6	1506	7	US-10-120-988-301	Sequence 301, App	C 908	12.4	88.6	2324	12	US-10-301-480-100707	Sequence 100707, A
C 836	12.4	88.6	1560	13	US-11-097-143-3380	Sequence 3380, App	C 909	12.4	88.6	2409	9	US-10-781-014-721	Sequence 721, App
C 837	12.4	88.6	1663	10	US-10-750-185-57070	Sequence 57070, A	C 910	12.4	88.6	2479	8	US-10-424-599-101161	Sequence 101161, A
C 838	12.4	88.6	1663	10	US-10-750-623-57070	Sequence 57070, A	C 911	12.4	88.6	2523	7	US-10-369-493-45949	Sequence 45949, A
C 839	12.4	88.6	1671	9	US-10-739-930-5100	Sequence 5100, App	C 912	12.4	88.6	2523	16	US-11-096-568A-24711	Sequence 24711, A
C 840	12.4	88.6	1692	8	US-10-755-889-661	Sequence 661, App	C 913	12.4	88.6	2535	10	US-10-450-763-25039	Sequence 25039, A
C 841	12.4	88.6	1710	8	US-10-767-701-13623	Sequence 13623, A	C 914	12.4	88.6	2535	13	US-11-097-143-40027	Sequence 40027, A
C 842	12.4	88.6	1729	9	US-10-494-672-339	Sequence 339, App	C 915	12.4	88.6	2721	10	US-10-764-420-2368	Sequence 2368, App
C 843	12.4	88.6	1749	7	US-09-369-493-34070	Sequence 34070, A	C 916	12.4	88.6	2725	6	US-10-087-192-188	Sequence 188, App
C 844	12.4	88.6	1771	4	US-09-925-065A-49840	Sequence 49840, A	C 917	12.4	88.6	2765	3	US-09-946-290-19	Sequence 19, App
C 845	12.4	88.6	1771	4	US-09-925-065A-49841	Sequence 49841, A	C 918	12.4	88.6	2811	8	US-10-425-114-27734	Sequence 27734, A
C 846	12.4	88.6	1771	4	US-09-925-065A-49842	Sequence 49842, A	C 919	12.4	88.6	2811	8	US-10-425-114-27734	Sequence 27734, A
C 847	12.4	88.6	1771	5	US-09-925-065A-49843	Sequence 49843, A	C 920	12.4	88.6	2888	9	US-10-425-115-35763	Sequence 35763, A
C 848	12.4	88.6	1771	5	US-09-925-065A-49844	Sequence 49844, A	C 921	12.4	88.6	3008	13	US-11-097-143-19417	Sequence 19417, A
C 849	12.4	88.6	1771	5	US-09-925-065A-49845	Sequence 49845, A	C 922	12.4	88.6	3014	8	US-10-425-114-31589	Sequence 31589, A
C 850	12.4	88.6	1771	12	US-10-301-480-151078	Sequence 151078, A	C 923	12.4	88.6	3050	9	US-10-473-126-29	Sequence 29, App
C 851	12.4	88.6	1771	12	US-10-301-480-151079	Sequence 151079, A	C 924	12.4	88.6	3083	13	US-11-097-143-27445	Sequence 27445, A
C 852	12.4	88.6	1771	12	US-10-301-480-151080	Sequence 151080, A	C 925	12.4	88.6	3125	13	US-11-097-143-40030	Sequence 40030, A
C 853	12.4	88.6	1771	12	US-10-301-480-764487	Sequence 764487, A	C 926	12.4	88.6	3129	3	US-09-938-842A-2286	Sequence 2286, App
C 854	12.4	88.6	1771	12	US-10-301-480-764488	Sequence 764488, A	C 927	12.4	88.6	3129	3	US-09-938-842A-2286	Sequence 2286, App
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C 856	12.4	88.6	1788	8	US-10-282-122A-8691	Sequence 8691, App	C 929	12.4	88.6	3130	5	US-09-925-065A-720418	Sequence 720418, A
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C 858	12.4	88.6	1830	10	US-10-750-185-42726	Sequence 42726, A	C 931	12.4	88.6	3131	8	US-10-437-963-101511	Sequence 101511, A
C 859	12.4	88.6	1830	10	US-10-750-623-42726	Sequence 42726, A	C 932	12.4	88.6	3162	13	US-11-097-143-610	Sequence 610, App
C 860	12.4	88.6	1836	3	US-09-864-761-16939	Sequence 16939, A	C 933	12.4	88.6	3209	10	US-10-450-763-28925	Sequence 28925, A
C 861	12.4	88.6	1863	7	US-10-369-493-34422	Sequence 34422, A	C 934	12.4	88.6	3237	16	US-11-096-568A-33584	Sequence 33584, A
C 862	12.4	88.6	1893	9	US-10-425-115-60177	Sequence 60177, A	C 935	12.4	88.6	3256	4	US-09-925-065A-688254	Sequence 688254, A
C 863	12.4	88.6	1907	9	US-10-767-795-1645	Sequence 1645, App	C 936	12.4	88.6	3256	5	US-09-925-065A-688254	Sequence 688254, A
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C 865	12.4	88.6	1932	8	US-10-437-963-101509	Sequence 101509, A	C 938	12.4	88.6	3290	8	US-10-437-963-3759	Sequence 3759, App
C 866	12.4	88.6	1942	10	US-10-750-185-31647	Sequence 31647, A	C 939	12.4	88.6	3304	8	US-10-437-963-24077	Sequence 24077, A
C 867	12.4	88.6	1942	10	US-10-750-623-31647	Sequence 31647, A	C 940	12.4	88.6	3328	13	US-11-097-143-24707	Sequence 24707, A
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C 869	12.4	88.6	1975	10	US-10-750-185-44865	Sequence 44865, A	C 942	12.4	88.6	3378	8	US-10-152-319A-1495	Sequence 1495, App
C 870	12.4	88.6	2031	6	US-10-750-623-44865	Sequence 44865, A	C 943	12.4	88.6	3378	16	US-11-036-136-1495	Sequence 1495, App
C 871	12.4	88.6	2031	6	US-10-750-623-258085	Sequence 258085, A	C 944	12.4	88.6	3398	8	US-10-437-963-88454	Sequence 88454, A
C 872	12.4	88.6	2031	7	US-10-027-632-258085	Sequence 258085, A	C 945	12.4	88.6	3621	9	US-10-425-115-144351	Sequence 144351, A
C 873	12.4	88.6	2031	12	US-10-301-480-92889	Sequence 92889, A	C 946	12.4	88.6	3621	13	US-11-097-143-3379	Sequence 3379, App
C 874	12.4	88.6	2031	12	US-10-301-480-706298	Sequence 706298, A	C 947	12.4	88.6	3777	10	US-10-467-657-5509	Sequence 5509, App
C 875	12.4	88.6	2046	9	US-10-377-139-20	Sequence 20, App	C 948	12.4	88.6	3800	8	US-10-398-221-3698	Sequence 3698, App
C 876	12.4	88.6	2049	10	US-10-750-185-40699	Sequence 40699, A	C 949	12.4	88.6	3800	8	US-10-398-221-3698	Sequence 3698, App
C 877	12.4	88.6	2049	10	US-10-750-623-40699	Sequence 40699, A	C 950	12.4	88.6	3854	8	US-10-282-122A-28925	Sequence 28925, A
C 878	12.4	88.6	2054	6	US-10-027-632-97584	Sequence 97584, A	C 951	12.4	88.6	3972	8	US-10-282-122A-29523	Sequence 29523, A
C 879	12.4	88.6	2054	6	US-10-027-632-99944	Sequence 99944, A	C 952	12.4	88.6	3979	7	US-10-275-026A-37	Sequence 37, App
C 880	12.4	88.6	2054	6	US-10-027-632-99945	Sequence 99945, A	C 953	12.4	88.6	4083	7	US-10-191-997-96	Sequence 96, App
C 881	12.4	88.6	2054	6	US-10-027-632-99946	Sequence 99946, A	C 954	12.4	88.6	4083	7	US-10-258-746-1	Sequence 1, App
C 882	12.4	88.6	2054	7	US-10-027-632-99944	Sequence 99944, A	C 955	12.4	88.6	4087	3	US-09-901-419-1	Sequence 1, App
C 883	12.4	88.6	2054	7	US-10-027-632-99944	Sequence 99944, A	C 956	12.4	88.6	4095	16	US-11-136-527-2030	Sequence 2030, App
C 884	12.4	88.6	2054	7	US-10-027-632-99945	Sequence 99945, A	C 957	12.4	88.6	4237	3	US-09-978-522-4	Sequence 4, App
C 885	12.4	88.6	2054	7	US-10-027-632-99946	Sequence 99946, A	C 958	12.4	88.6	4371	10	US-10-450-763-7102	Sequence 7102, App
C 886	12.4	88.6	2054	8	US-10-027-632-99946	Sequence 99946, A	C 959	12.4	88.6	4371	10	US-10-450-763-24505	Sequence 24505, A
C 887	12.4	88.6	2079	11	US-10-933-182A-82278	Sequence 82278, A	C 960	12.4	88.6	4371	10	US-10-450-763-26898	Sequence 26898, A
C 888	12.4	88.6	2082	8	US-10-424-599-91349	Sequence 91349, A	C 961	12.4	88.6	4550	3	US-09-853-526-182	Sequence 182, App
C 889	12.4	88.6	2083	10	US-10-887-553A-883	Sequence 883, App	C 962	12.4	88.6	4683	3	US-09-070-927A-193	Sequence 193, App
C 890	12.4	88.6	2133	3	US-09-738-626-590	Sequence 590, App	C 963	12.4	88.6	4687	3	US-09-978-522-2	Sequence 2, App
C 891	12.4	88.6	2147	10	US-10-750-185-32983	Sequence 32983, A	C 964	12.4	88.6	4754	13	US-11-097-143-7390	Sequence 7390, App
C 892	12.4	88.6	2147	10	US-10-750-623-32983	Sequence 32983, A	C 965	12.4	88.6	4883	6	US-10-128-714-429	Sequence 429, App
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967 12.4 88.6 5438 9 US-10-357-930-24294 Sequence 24294, A
968 12.4 88.6 5761 10 US-10-486-706-259 Sequence 259, App
969 12.4 88.6 5816 10 US-10-764-420-2097 Sequence 2097, Ap
970 12.4 88.6 5977 9 US-10-331-053-82 Sequence 82, Appl
971 12.4 88.6 6106 7 US-10-062-674-1648 Sequence 1648, Ap
972 12.4 88.6 7139 13 US-11-097-143-12904 Sequence 12904, A
973 12.4 88.6 7327 10 US-10-496-011-17 Sequence 17, Appl
974 12.4 88.6 7358 13 US-11-097-143-24706 Sequence 24706, A
975 12.4 88.6 7642 3 US-09-938-842A-43 Sequence 43, Appl
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977 12.4 88.6 7898 10 US-10-483-467-3 Sequence 3, Appli
978 12.4 88.6 10024 3 US-09-880-107-2430 Sequence 2430, Ap
979 12.4 88.6 11831 2 US-08-961-527-65 Sequence 65, Appl
980 12.4 88.6 11841 8 US-10-158-844-65 Sequence 65, Appl
981 12.4 88.6 17042 10 US-10-965-566-5 Sequence 5, Appli
982 12.4 88.6 21142 10 US-10-995-561-13380 Sequence 13380, A
983 12.4 88.6 21739 8 US-10-741-601-5713 Sequence 5713, Ap
984 12.4 88.6 21739 9 US-10-741-600-17817 Sequence 17817, A
985 12.4 88.6 21791 16 US-11-124-367A-5061 Sequence 5061, Ap
986 12.4 88.6 22477 6 US-10-087-192-1594 Sequence 1594, Ap
987 12.4 88.6 29829 6 US-10-087-192-694 Sequence 694, App
988 12.4 88.6 32070 9 US-10-741-600-17732 Sequence 17732, A
989 12.4 88.6 32070 10 US-10-995-561-13317 Sequence 13317, A
990 12.4 88.6 32134 3 US-09-764-847-1057 Sequence 1057, Ap
991 12.4 88.6 32134 3 US-09-764-877-3535 Sequence 3535, Ap
992 12.4 88.6 32134 3 US-09-764-891-6357 Sequence 6357, Ap
993 12.4 88.6 32134 6 US-10-092-154-1057 Sequence 1057, Ap
994 12.4 88.6 32134 6 US-10-205-428-653 Sequence 653, App
995 12.4 88.6 32134 7 US-10-242-515-3535 Sequence 3535, Ap
996 12.4 88.6 32187 3 US-09-764-847-1550 Sequence 1550, Ap
997 12.4 88.6 32187 6 US-10-092-154-1550 Sequence 1550, Ap
998 12.4 88.6 32193 3 US-09-764-847-1549 Sequence 1549, Ap
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ALIGNMENTS

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RESULT 1
US-09-865-579A-17
; Sequence 17, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiko
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
US-09-865-579A-17
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Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTTAC 14
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Db 1 GAAGGTGTGCTTAC 14
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US-09-865-579A-19
; Sequence 19, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiko
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-19
Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTTAC 14
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Db 1 GAAGGTGTGCTTAC 14
RESULT 3
US-10-735-357-44/c
; Sequence 44, Application US/10735357
; Publication No. US20050059030A1
; GENERAL INFORMATION:
; APPLICANT: Bao, Yijia P.
; APPLICANT: Marla, Sudhakar S.
; APPLICANT: Muller, Uwe
; APPLICANT: Storchoff, James J.
; APPLICANT: Hagenow, Susan R.
; TITLE OF INVENTION: Direct SNP Detection with Unamplified DNA
; FILE REFERENCE: 02-1227-A
; CURRENT APPLICATION NUMBER: US/10/735,357
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/432,772
; PRIOR FILING DATE: 2002-12-12
; PRIOR APPLICATION NUMBER: US 60/433,442
; PRIOR FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-735-357-44
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Query Match 100.0%; Score 14; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTTAC 14
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Db 20 GAAGGTGTGCTTAC 7

RESULT 4

US-10-735-357-75

; Sequence 75, Application US/10735357

; Publication No. US20050059030A1

; GENERAL INFORMATION:

; APPLICANT: Bao, Yijia P.

; APPLICANT: Maria, Sudhakar S.

; APPLICANT: Muller, Uwe

; APPLICANT: Storhoff, James J.

; APPLICANT: Hagenow, Susan R.

; TITLE OF INVENTION: Direct SNP Detection with Unamplified DNA

; FILE REFERENCE: 02-1227-A

; CURRENT APPLICATION NUMBER: US/10/735,357

; PRIOR FILING DATE: 2003-12-12

; PRIOR APPLICATION NUMBER: US 60/432,772

; PRIOR FILING DATE: 2002-12-12

; PRIOR APPLICATION NUMBER: US 60/433,442

; PRIOR FILING DATE: 2002-12-12

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 75

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide

US-10-735-357-75

Query Match

Best Local Similarity 100.0%; Score 14; DB 10; Length 22;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

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Db 3 GAAGGTGTGCTTAC 16

RESULT 5

US-10-995-051-16/c

; Sequence 16, Application US/10995051

; Publication No. US20050250094A1

; GENERAL INFORMATION:

; APPLICANT: Storhoff, James

; APPLICANT: Lucas, Adam

; APPLICANT: Muller, Uwe

; APPLICANT: Bao, Yijia P

; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination

; FILE REFERENCE: MBHB-03-466-E

; CURRENT APPLICATION NUMBER: US/10/995,051

; PRIOR FILING DATE: 2004-11-22

; PRIOR APPLICATION NUMBER: 10/854,848

; PRIOR FILING DATE: 2004-05-27

; PRIOR APPLICATION NUMBER: 60/474,569

; PRIOR FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 60/499,034

; PRIOR FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 60/517,450

; PRIOR FILING DATE: 2003-11-04

; PRIOR APPLICATION NUMBER: 60/567,874

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 16

; LENGTH: 22

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Probe meca 4 for the meca gene.

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(1)

; OTHER INFORMATION: g is linked to SEQ ID NO: 32 by polyethylene glycol

US-10-995-051-16

Query Match

Best Local Similarity 100.0%; Score 14; DB 10; Length 22;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

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Db 20 GAAGGTGTGCTTAC 7

RESULT 6

US-10-995-051-14/c

; Sequence 14, Application US/10995051

; Publication No. US20050250094A1

; GENERAL INFORMATION:

; APPLICANT: Storhoff, James

; APPLICANT: Lucas, Adam

; APPLICANT: Muller, Uwe

; APPLICANT: Bao, Yijia P

; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination

; FILE REFERENCE: MBHB-03-466-E

; CURRENT APPLICATION NUMBER: US/10/995,051

; PRIOR FILING DATE: 2004-11-22

; PRIOR APPLICATION NUMBER: 10/854,848

; PRIOR FILING DATE: 2004-05-27

; PRIOR APPLICATION NUMBER: 60/474,569

; PRIOR FILING DATE: 2003-05-30

; PRIOR APPLICATION NUMBER: 60/499,034

; PRIOR FILING DATE: 2003-08-29

; PRIOR APPLICATION NUMBER: 60/517,450

; PRIOR FILING DATE: 2003-11-04

; PRIOR APPLICATION NUMBER: 60/567,874

; PRIOR FILING DATE: 2004-05-03

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 14

; LENGTH: 281

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Target Meca 4 is a meca 281 base-pair PCR amplicon.

US-10-995-051-14

Query Match

Best Local Similarity 100.0%; Score 14; DB 10; Length 281;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

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Db 47 GAAGGTGTGCTTAC 34

RESULT 7

US-10-478-633A-151/c

; Sequence 151, Application US/10478633A

; Publication No. US20050059000A1

; GENERAL INFORMATION:

; APPLICANT: TAKARA BIO INC.

; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for

; FILE REFERENCE: 663232

; CURRENT APPLICATION NUMBER: US/10/478,633A

; PRIOR FILING DATE: 2003-11-25

; PRIOR APPLICATION NUMBER: JP 2001-177737

; PRIOR FILING DATE: 2001-06-12

; PRIOR APPLICATION NUMBER: JP 2001-249689

; PRIOR FILING DATE: 2001-08-20

; NUMBER OF SEQ ID NOS: 173

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; SEQ ID NO 151
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-151

Query Match      100.0%; Score 14; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      74 GAAGGTGTGCTTAC 61

RESULT 8
US-10-027-632-152712
; Sequence 152712, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152712
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152712

Query Match      100.0%; Score 14; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      699 GAAGGTGTGCTTAC 712

RESULT 9
US-10-027-632-152713
; Sequence 152713, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
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; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152713
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152713

Query Match      100.0%; Score 14; DB 6; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      699 GAAGGTGTGCTTAC 712

RESULT 10
US-10-027-632-152712
; Sequence 152712, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152712
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-152712

Query Match      100.0%; Score 14; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTAC 14
Db      699 GAAGGTGTGCTTAC 712

RESULT 11
US-10-027-632-152713
; Sequence 152713, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
```

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS in the Human Genome

FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 152713

LENGTH: 738

TYPE: DNA

ORGANISM: Human

US-10-027-632-152713

Query Match 100.0%; Score 14; DB 7; Length 738;

Best Local Similarity 100.0%; Pred. No. 9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14

DB 699 GAAGGTGCTTAC 712

RESULT 12

US-10-425-114-2665/c

Sequence 2665, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 2665

LENGTH: 1502

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700220675_FLI

US-10-425-114-2665

Query Match 100.0%; Score 14; DB 8; Length 1502;

Best Local Similarity 100.0%; Pred. No. 9.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14

DB 618 GAAGGTGCTTAC 605

RESULT 13

US-10-425-115-102549/c

Sequence 102549, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

PLANTS

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 102549

LENGTH: 1502

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_25033C.1

US-10-425-115-102549

Query Match 100.0%; Score 14; DB 9; Length 1502;

Best Local Similarity 100.0%; Pred. No. 9.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14

DB 1044 GAAGGTGCTTAC 1031

RESULT 15

US-09-452-599-169/c

Sequence 169, Application US/09452599

Patent No. US20020055101A1

GENERAL INFORMATION:

APPLICANT: Bergeron, Michel G.

APPLICANT: Ouellette, Marc

APPLICANT: Roy, Paul H.

TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers

TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL

PATHOGENS AND ANTIBIOTIC RESISTANCE GENES FROM CLINICAL

SPECIMENS FOR ROUTINE DIAGNOSIS IN MICRO

ORGANISMS

; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 14; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 16

US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 14; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 17

US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match 100.0%; Score 14; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 18

US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match 100.0%; Score 14; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14
|||
Db 1094 GAAGGTGTGCTTAC 1081

RESULT 19

US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match 100.0%; Score 14; DB 9; Length 2007;

Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1094 GAAGGTGTGCTTAC 1081

RESULT 20

US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 14; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1094 GAAGGTGTGCTTAC 1081

RESULT 21

US-10-320-797-1231/c
; Sequence 1231, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1231
; LENGTH: 2015
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
US-10-320-797-1231

Query Match 100.0%; Score 14; DB 8; Length 2015;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1034 GAAGGTGTGCTTAC 1021

RESULT 22

US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match 100.0%; Score 14; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 9.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 1115 GAAGGTGTGCTTAC 1102

RESULT 23

US-10-320-797-231/c
; Sequence 231, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 231
; LENGTH: 4015
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
US-10-320-797-231

Query Match 100.0%; Score 14; DB 8; Length 4015;
Best Local Similarity 100.0%; Pred. No. 9.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 2034 GAAGGTGTGCTTAC 2021

RESULT 24

US-10-719-900-225680/c
; Sequence 225680, Application US/10719900

```
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 225680
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-225680

Query Match          92.9%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 14 GAAGGTGTGCTTA 2

RESULT 25
US-11-036-317-858913
; Sequence 858913, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 858913
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-858913

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 8 AAGGTGTGCTTAC 20

RESULT 26
US-11-036-317-863503
; Sequence 863503, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 863503
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-863503

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 6 AAGGTGTGCTTAC 18

RESULT 27
US-11-036-317-888398
; Sequence 888398, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 888398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-888398

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 9 AAGGTGTGCTTAC 21

RESULT 28
US-11-036-317-958076
; Sequence 958076, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 958076
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-958076

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 6 AAGGTGTGCTTAC 18

Query Match          92.9%; Score 13; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 29
US-10-741-601-18514
; Sequence 18514, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18514
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-18514

Query Match          92.9%; Score 13; DB 8; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 38 GAAGGTGTGCTTA 50

RESULT 30
US-10-741-600-50241
; Sequence 50241, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50241
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-50241

Query Match          92.9%; Score 13; DB 9; Length 201;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 38 GAAGGTGTGCTTA 50

RESULT 31
US-10-450-763-29551
; Sequence 29551, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
```

```
; SOFTWARE: Custom
; SEQ ID NO 29551
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (78)..(116)
; OTHER INFORMATION: 84% homologous to Escherichia coli rtn, accession number
; OTHER INFORMATION: U83404, Smith-Waterman Score=64.
US-10-450-763-29551

Query Match          92.9%; Score 13; DB 10; Length 301;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
Db 132 AAGGTGTGCTTAC 144

RESULT 32
US-10-424-599-6873/c
; Sequence 6873, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 6873
; LENGTH: 335
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106214C.1
US-10-424-599-6873

Query Match          92.9%; Score 13; DB 8; Length 335;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
Db 21 GAAGGTGTGCTTA 9

RESULT 33
US-09-732-627A-1859
; Sequence 1859, Application US/09732627A
; Publication No. US20040123338A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen L.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51770)B
; CURRENT APPLICATION NUMBER: US/09/732,627A
; CURRENT FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 4930
; SEQ ID NO 1859
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(339)
; OTHER INFORMATION: unsure at all n locations
```

```
/ OTHER INFORMATION: Clone ID: LIB3493-052-F1-M1-C7
US-09-732-627A-1859

Query Match          92.9%; Score 13; DB 3; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 13
    |||||
Db 43 GAAGGTGTGCTTAC 55

RESULT 34
US-10-424-599-129096/c
; Sequence 129096, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 129096
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(346)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_87579C.1
US-10-424-599-129096

Query Match          92.9%; Score 13; DB 8; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 202 AAGGTGTGCTTAC 190

RESULT 35
US-09-925-065A-201193
; Sequence 201193, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201193
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
```

```
/ TYPE: DNA
US-09-925-065A-201193

Query Match          92.9%; Score 13; DB 4; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 89 AAGGTGTGCTTAC 101

RESULT 36
US-09-925-065A-201193
; Sequence 201193, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201193
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-925-065A-201193

Query Match          92.9%; Score 13; DB 5; Length 418;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
    |||||
Db 89 AAGGTGTGCTTAC 101

RESULT 37
US-09-925-065A-201194
; Sequence 201194, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201194
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201194

Query Match 92.9%; Score 13; DB 4; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
|||||
Db 102 AAGGTGTGCTTAC 114

RESULT 38
US-09-925-065A-201194
; Sequence 201194, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 201194
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-201194

Query Match 92.9%; Score 13; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
|||||
Db 102 AAGGTGTGCTTAC 114

RESULT 39
US-10-301-480-289751
; Sequence 289751, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 289751
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-158432/c

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-289751

Query Match 92.9%; Score 13; DB 12; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
|||||
Db 103 AAGGTGTGCTTAC 115

RESULT 40
US-10-301-480-903160
; Sequence 903160, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 903160
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-903160

Query Match 92.9%; Score 13; DB 12; Length 427;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
|||||
Db 103 AAGGTGTGCTTAC 115

RESULT 41
US-09-925-065A-158432/c
; Sequence 158432, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 158432
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-158432

Query Match 92.9%; Score 13; DB 4; Length 443;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
 |||||
 Db 117 GAAGGTGTGCTTA 105

RESULT 42
 US-09-925-065A-158432/c
 ; Sequence 158432, Application US/09925065A
 ; Publication No. US20050228172A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: 108927.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 158432
 ; LENGTH: 443
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-925-065A-158432

Query Match 92.9%; Score 13; DB 5; Length 443;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
 |||||
 Db 117 GAAGGTGTGCTTA 105

RESULT 43
 US-10-437-963-95228
 ; Sequence 95228, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 95228
 ; LENGTH: 459
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_93443C.1

US-10-437-963-95228

Query Match 92.9%; Score 13; DB 8; Length 459;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
 |||||
 Db 42 AAGGTGTGCTTAC 54

RESULT 44
 US-10-437-963-49273
 ; Sequence 49273, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 49273
 ; LENGTH: 467
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_51871C.1
 US-10-437-963-49273

Query Match 92.9%; Score 13; DB 8; Length 467;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
 |||||
 Db 119 GAAGGTGTGCTTA 131

RESULT 45
 US-09-925-065A-282736
 ; Sequence 282736, Application US/09925065A
 ; Publication No. US20040181048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single
 ; FILE REFERENCE: 108927.135
 ; CURRENT APPLICATION NUMBER: US/09/925,065A
 ; CURRENT FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: US 60/243,096
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 60/252,147
 ; PRIOR FILING DATE: 2000-11-20
 ; PRIOR APPLICATION NUMBER: US 60/250,092
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: US 60/261,766
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/289,846
 ; PRIOR FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 957086
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 282736
 ; LENGTH: 468
 ; TYPE: DNA

```
; ORGANISM: Homo sapiens
US-09-925-065A-282736

Query Match          92.9%; Score 13; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTA 13
Db      128 GAAGGTGTGCTTA 140

RESULT 46
US-09-925-065A-515582/c
; Sequence 515582, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 515582
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-515582

Query Match          92.9%; Score 13; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTA 13
Db      128 GAAGGTGTGCTTA 140

RESULT 47
US-09-925-065A-282736
; Sequence 282736, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282736
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-282736

Query Match          92.9%; Score 13; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTA 13
Db      128 GAAGGTGTGCTTA 140

RESULT 48
US-09-925-065A-515582/c
; Sequence 515582, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 515582
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-515582

Query Match          92.9%; Score 13; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTA 13
Db      431 GAAGGTGTGCTTA 419

RESULT 49
US-10-301-480-359684
; Sequence 359684, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359684
; LENGTH: 474
; TYPE: DNA
```

```
; SEQ ID NO 282736
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-282736

Query Match          92.9%; Score 13; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAAGGTGTGCTTA 13
Db      128 GAAGGTGTGCTTA 140

RESULT 48
US-09-925-065A-515582/c
; Sequence 515582, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 468
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-515582

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 359684, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US 10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 359684
; LENGTH: 474
; TYPE: DNA
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; ORGANISM: Homo sapien
US-10-301-480-359684

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 973093, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
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; ORGANISM: Homo sapien
US-10-301-480-973093

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Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       134 GAAGGTGTGCTTA 146

Search completed: May 31, 2006, 22:06:45
Job time : 1490 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:42:13 ; Search time 57 Seconds
(without alignments)
28.927 Million cell updates/sec

Title: US-09-865-579a-19

Perfect score: 14

Sequence: 1 gaaggtgcttac 14

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications NA New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	12.4	88.6	50	US-10-511-937-2635	Sequence 2635, Ap
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C 3	12.4	88.6	1019	US-10-953-349-20394	Sequence 20394, A
C 4	12.4	88.6	1161	US-11-217-529-3002	Sequence 3002, Ap
C 5	12.4	88.6	1304	US-10-953-349-8649	Sequence 8649, Ap
C 6	12.4	88.6	1451	US-10-511-937-2804	Sequence 2804, Ap
C 7	12.4	88.6	2079	US-11-217-529-82278	Sequence 82278, A
C 8	12.4	88.6	3435	US-10-953-349-4556	Sequence 4556, Ap
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C 10	12	85.7	650	US-10-953-349-23971	Sequence 23971, A
C 11	12	85.7	651	US-10-953-349-12654	Sequence 12654, A
C 12	12	85.7	951	US-11-217-529-2897	Sequence 2897, A
C 13	12	85.7	1212	US-10-953-349-17567	Sequence 17567, A
C 14	12	85.7	1578	US-11-024-544A-17	Sequence 17, Appl
C 15	12	85.7	1578	US-11-190-750-131	Sequence 131, App
C 16	12	85.7	1578	US-11-264-784-83	Sequence 83, Appl
C 17	12	85.7	1578	US-11-264-737-124	Sequence 124, App
C 18	12	85.7	1584	US-11-217-529-84407	Sequence 84407, A
C 19	12	85.7	1667	US-10-953-349-12369	Sequence 12369, A
C 20	12	85.7	1683	US-11-024-544A-156	Sequence 156, App
C 21	12	85.7	1683	US-11-190-750-127	Sequence 127, App
C 22	12	85.7	1749	US-10-953-349-16812	Sequence 16812, A
C 23	12	85.7	1841	US-11-145-307A-163	Sequence 163, App
C 24	12	85.7	3915	US-11-217-529-2644	Sequence 2644, Ap
C 25	12	85.7	8666	US-11-024-544A-165	Sequence 165, App

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Sequence 21401, A
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Sequence 11605, A
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Sequence 90, Appl
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c 153	10.8	77.1	756	7	US-11-217-529-4019	Sequence 4019, Ap	c 226	10.8	77.1	1512	7	US-11-217-529-76442	Sequence 76442, A
c 154	10.8	77.1	760	6	US-10-953-349-28024	Sequence 28024, A	c 227	10.8	77.1	1530	7	US-11-217-529-2013	Sequence 2013, Ap
c 155	10.8	77.1	777	7	US-11-217-529-80790	Sequence 80790, A	c 228	10.8	77.1	1535	6	US-11-217-529-15855	Sequence 15855, A
c 156	10.8	77.1	783	7	US-11-217-529-800	Sequence 800, App	c 229	10.8	77.1	1540	6	US-10-953-349-26656	Sequence 26656, A
c 157	10.8	77.1	783	7	US-11-217-529-1054	Sequence 1054, Ap	c 230	10.8	77.1	1542	7	US-11-181-115-21	Sequence 21, Appl
c 158	10.8	77.1	787	7	US-11-217-529-75859	Sequence 75859, A	c 231	10.8	77.1	1544	6	US-10-953-349-4088	Sequence 4088, Ap
c 159	10.8	77.1	807	6	US-10-488-619-2354	Sequence 2354, Ap	c 232	10.8	77.1	1544	6	US-10-953-349-29884	Sequence 29884, A
c 160	10.8	77.1	810	7	US-11-217-529-965	Sequence 965, App	c 233	10.8	77.1	1564	7	US-11-293-697-1059	Sequence 1059, Ap
c 161	10.8	77.1	816	6	US-10-953-349-35070	Sequence 35070, A	c 234	10.8	77.1	1567	7	US-10-953-349-3744	Sequence 3744, A
c 162	10.8	77.1	828	6	US-10-953-349-16551	Sequence 16551, A	c 235	10.8	77.1	1641	6	US-10-953-349-40249	Sequence 40249, A
c 163	10.8	77.1	836	6	US-10-953-349-1414	Sequence 1414, A	c 236	10.8	77.1	1641	6	US-11-217-529-81956	Sequence 81956, A
c 164	10.8	77.1	850	6	US-10-953-349-15270	Sequence 15270, A	c 237	10.8	77.1	1650	7	US-11-293-697-63	Sequence 63, Appl
c 165	10.8	77.1	855	6	US-10-514-535-1	Sequence 1, Appl	c 238	10.8	77.1	1684	7	US-10-953-349-32444	Sequence 32444, A
c 166	10.8	77.1	861	7	US-11-217-529-78673	Sequence 78673, A	c 239	10.8	77.1	1695	6	US-10-953-349-36924	Sequence 36924, A
c 167	10.8	77.1	865	6	US-10-953-349-8546	Sequence 8546, Ap	c 240	10.8	77.1	1706	7	US-10-953-349-36924	Sequence 36924, A
c 168	10.8	77.1	870	6	US-10-953-349-139	Sequence 139, App	c 241	10.8	77.1	1719	7	US-11-217-529-76843	Sequence 76843, A
c 169	10.8	77.1	870	7	US-11-101-316-25	Sequence 25, Appl	c 242	10.8	77.1	1719	7	US-11-217-529-80736	Sequence 80736, A
c 170	10.8	77.1	875	6	US-10-514-535-2	Sequence 2, Appl	c 243	10.8	77.1	1720	6	US-10-953-349-32176	Sequence 32176, A
c 171	10.8	77.1	897	7	US-11-217-529-2796	Sequence 2796, Ap	c 244	10.8	77.1	1722	7	US-11-217-529-3909	Sequence 3909, Ap

c 245	10.8	77.1	1725	7	US-11-121-154-50	Sequence 50, Appl	318	10.8	77.1	5920	7	US-11-145-307A-185	Sequence 185, App
c 246	10.8	77.1	1750	6	US-10-953-349-34792	Sequence 34792, A	c 319	10.8	77.1	6321	6	US-10-713-648A-22	Sequence 22, Appl
c 247	10.8	77.1	1767	6	US-10-953-349-8450	Sequence 8450, App	c 320	10.8	77.1	6321	6	US-10-713-648A-5	Sequence 5, Appl
c 248	10.8	77.1	1785	7	US-11-217-529-77319	Sequence 77319, A	c 321	10.8	77.1	10574	7	US-11-267-871-719	Sequence 719, App
c 249	10.8	77.1	1797	7	US-11-217-529-80787	Sequence 80787, A	c 322	10.8	77.1	135090	6	US-10-505-928-607	Sequence 607, App
c 250	10.8	77.1	1803	7	US-11-217-529-2767	Sequence 2767, App	c 323	10.8	77.1	394191	6	US-10-506-549-3	Sequence 3, Appl
c 251	10.8	77.1	1810	6	US-10-953-349-10986	Sequence 10986, A	c 324	10.4	74.3	22	7	US-11-248-986-23	Sequence 23, Appl
c 252	10.8	77.1	1866	7	US-11-121-154-10	Sequence 10, Appl	c 325	10.4	74.3	25	7	US-11-217-529-16665	Sequence 16665, A
c 253	10.8	77.1	1878	7	US-11-217-529-1367	Sequence 1367, App	c 326	10.4	74.3	25	7	US-11-217-529-19558	Sequence 19558, A
c 254	10.8	77.1	1878	7	US-11-217-529-2508	Sequence 2508, App	c 327	10.4	74.3	25	7	US-11-217-529-20016	Sequence 20016, A
c 255	10.8	77.1	1880	6	US-10-953-349-29344	Sequence 29344, A	c 328	10.4	74.3	25	7	US-11-217-529-20081	Sequence 20081, A
c 256	10.8	77.1	1896	6	US-10-953-349-26191	Sequence 26191, A	c 329	10.4	74.3	25	7	US-11-217-529-21404	Sequence 21404, A
c 257	10.8	77.1	1950	7	US-11-217-529-3485	Sequence 3485, App	c 330	10.4	74.3	25	7	US-11-217-529-106469	Sequence 106469, A
c 258	10.8	77.1	1968	7	US-11-293-697-2283	Sequence 2283, App	c 331	10.4	74.3	25	7	US-11-217-529-107771	Sequence 107771, A
c 259	10.8	77.1	2070	6	US-10-509-131-37	Sequence 37, Appl	c 332	10.4	74.3	25	7	US-11-217-529-110946	Sequence 110946, A
c 260	10.8	77.1	2117	7	US-11-293-697-573	Sequence 573, App	c 333	10.4	74.3	25	7	US-11-217-529-121489	Sequence 121489, A
c 261	10.8	77.1	2142	7	US-11-217-529-36	Sequence 36, Appl	c 334	10.4	74.3	25	7	US-11-217-529-149644	Sequence 149644, A
c 262	10.8	77.1	2178	7	US-11-217-529-191034	Sequence 191034, A	c 335	10.4	74.3	25	7	US-11-217-529-153219	Sequence 153219, A
c 263	10.8	77.1	2181	7	US-11-293-697-1647	Sequence 1647, App	c 336	10.4	74.3	25	7	US-11-217-529-176667	Sequence 176667, A
c 264	10.8	77.1	2184	7	US-11-217-529-166643	Sequence 166643, A	c 337	10.4	74.3	25	7	US-11-217-529-176669	Sequence 176669, A
c 265	10.8	77.1	2267	7	US-11-217-529-77716	Sequence 77716, A	c 338	10.4	74.3	25	7	US-11-217-529-176672	Sequence 176672, A
c 266	10.8	77.1	2267	7	US-11-266-446-40	Sequence 40, Appl	c 339	10.4	74.3	25	7	US-11-217-529-176674	Sequence 176674, A
c 267	10.8	77.1	2287	7	US-11-293-697-1973	Sequence 1973, App	c 340	10.4	74.3	51	7	US-11-245-248-272	Sequence 272, App
c 268	10.8	77.1	2356	7	US-11-293-697-1705	Sequence 1705, App	c 341	10.4	74.3	93	7	US-11-217-529-173314	Sequence 173314, A
c 269	10.8	77.1	2363	7	US-11-293-697-1688	Sequence 1688, App	c 342	10.4	74.3	144	7	US-11-217-529-3905	Sequence 3905, App
c 270	10.8	77.1	2366	6	US-10-196-749-309	Sequence 309, App	c 343	10.4	74.3	151	7	US-11-320-481-16	Sequence 16, Appl
c 271	10.8	77.1	2436	7	US-11-101-316-99	Sequence 99, Appl	c 344	10.4	74.3	197	6	US-10-473-173-476	Sequence 476, App
c 272	10.8	77.1	2460	7	US-11-217-529-174454	Sequence 174454, A	c 345	10.4	74.3	288	7	US-11-217-529-263	Sequence 263, App
c 273	10.8	77.1	2463	7	US-11-293-697-5	Sequence 5, Appl	c 346	10.4	74.3	317	6	US-10-488-619-1102	Sequence 1102, App
c 274	10.8	77.1	2492	7	US-11-293-697-1721	Sequence 1721, App	c 347	10.4	74.3	318	7	US-11-321-475-7	Sequence 7, Appl
c 275	10.8	77.1	2529	7	US-11-217-529-4657	Sequence 4657, App	c 348	10.4	74.3	354	7	US-11-217-529-77859	Sequence 77859, A
c 276	10.8	77.1	2536	7	US-11-293-697-1295	Sequence 1295, App	c 349	10.4	74.3	354	7	US-11-217-529-78681	Sequence 78681, A
c 277	10.8	77.1	2540	7	US-11-121-154-36	Sequence 36, Appl	c 350	10.4	74.3	363	7	US-11-217-529-81538	Sequence 81538, A
c 278	10.8	77.1	2547	6	US-10-953-349-9185	Sequence 9185, App	c 351	10.4	74.3	374	6	US-10-488-619-1951	Sequence 1951, App
c 279	10.8	77.1	2589	7	US-11-121-154-38	Sequence 38, Appl	c 352	10.4	74.3	399	7	US-11-217-529-81634	Sequence 81634, A
c 280	10.8	77.1	2659	7	US-11-293-697-616	Sequence 616, App	c 353	10.4	74.3	402	6	US-10-488-619-742	Sequence 742, App
c 281	10.8	77.1	2719	7	US-11-293-697-1193	Sequence 1193, App	c 354	10.4	74.3	405	7	US-11-217-529-81704	Sequence 81704, A
c 282	10.8	77.1	2751	7	US-11-293-697-8153	Sequence 8153, App	c 355	10.4	74.3	434	7	US-11-301-554-1480	Sequence 1480, App
c 283	10.8	77.1	2822	6	US-10-953-349-9753	Sequence 9753, App	c 356	10.4	74.3	486	7	US-11-217-529-166749	Sequence 166749, A
c 284	10.8	77.1	2823	7	US-11-217-529-4032	Sequence 4032, App	c 357	10.4	74.3	488	6	US-10-953-349-36206	Sequence 36206, A
c 285	10.8	77.1	2826	7	US-11-293-697-2347	Sequence 2347, App	c 358	10.4	74.3	491	6	US-10-488-619-624	Sequence 624, App
c 286	10.8	77.1	2875	7	US-11-293-697-613	Sequence 613, App	c 359	10.4	74.3	510	7	US-11-301-554-567	Sequence 567, App
c 287	10.8	77.1	2867	6	US-10-953-349-8439	Sequence 8439, App	c 360	10.4	74.3	522	7	US-11-217-529-81632	Sequence 81632, A
c 288	10.8	77.1	2985	6	US-10-953-349-32829	Sequence 32829, App	c 361	10.4	74.3	549	7	US-11-217-529-1910	Sequence 1910, App
c 289	10.8	77.1	2988	7	US-11-217-529-2172	Sequence 2172, App	c 362	10.4	74.3	585	6	US-10-488-619-1220	Sequence 1220, App
c 290	10.8	77.1	3032	6	US-10-514-535-7	Sequence 7, Appl	c 363	10.4	74.3	605	6	US-10-473-173-313	Sequence 313, App
c 291	10.8	77.1	3161	7	US-11-293-697-1992	Sequence 1992, App	c 364	10.4	74.3	609	7	US-11-217-529-82003	Sequence 82003, A
c 292	10.8	77.1	3190	7	US-11-293-697-323	Sequence 323, App	c 365	10.4	74.3	630	6	US-10-953-349-26350	Sequence 26350, A
c 293	10.8	77.1	3219	7	US-11-217-529-82170	Sequence 82170, A	c 366	10.4	74.3	642	7	US-11-217-529-78763	Sequence 78763, A
c 294	10.8	77.1	3225	7	US-11-217-529-77049	Sequence 77049, A	c 367	10.4	74.3	648	7	US-11-217-529-1283	Sequence 1283, App
c 295	10.8	77.1	3239	6	US-10-505-928-294	Sequence 294, App	c 368	10.4	74.3	660	7	US-11-217-529-570	Sequence 570, App
c 296	10.8	77.1	3243	7	US-11-217-529-80372	Sequence 80372, A	c 369	10.4	74.3	663	7	US-11-226-605-47	Sequence 47, Appl
c 297	10.8	77.1	3252	7	US-11-293-697-604	Sequence 604, App	c 370	10.4	74.3	663	7	US-11-217-529-78680	Sequence 78680, A
c 298	10.8	77.1	3357	7	US-11-217-529-80104	Sequence 80104, A	c 371	10.4	74.3	666	6	US-10-953-349-8273	Sequence 8273, App
c 299	10.8	77.1	3364	7	US-11-293-697-1320	Sequence 1320, App	c 372	10.4	74.3	667	6	US-10-488-619-2859	Sequence 2859, App
c 300	10.8	77.1	3374	6	US-10-514-535-5	Sequence 5, Appl	c 373	10.4	74.3	669	6	US-10-473-173-31	Sequence 31, Appl
c 301	10.8	77.1	3485	7	US-11-145-307A-192	Sequence 192, App	c 374	10.4	74.3	678	7	US-11-217-529-75902	Sequence 75902, A
c 302	10.8	77.1	3578	6	US-10-509-131-49	Sequence 49, Appl	c 375	10.4	74.3	701	6	US-10-488-619-2098	Sequence 2098, App
c 303	10.8	77.1	3585	7	US-11-217-529-1567	Sequence 1567, App	c 376	10.4	74.3	702	7	US-11-217-529-4708	Sequence 4708, App
c 304	10.8	77.1	3733	6	US-10-514-535-3	Sequence 3, Appl	c 377	10.4	74.3	704	7	US-11-301-554-206	Sequence 206, App
c 305	10.8	77.1	3743	6	US-10-502-993-1	Sequence 1, Appl	c 378	10.4	74.3	708	6	US-10-953-349-14041	Sequence 14041, A
c 306	10.8	77.1	3780	6	US-10-509-131-24	Sequence 24, Appl	c 379	10.4	74.3	716	6	US-10-953-349-30224	Sequence 30224, A
c 307	10.8	77.1	3786	7	US-11-293-697-436	Sequence 436, App	c 380	10.4	74.3	724	6	US-10-953-349-15117	Sequence 15117, A
c 308	10.8	77.1	3787	6	US-10-514-535-4	Sequence 4, Appl	c 381	10.4	74.3	732	7	US-11-217-529-81607	Sequence 81607, A
c 309	10.8	77.1	3801	7	US-11-217-529-4511	Sequence 4511, App	c 382	10.4	74.3	748	6	US-10-488-619-2227	Sequence 2227, App
c 310	10.8	77.1	4008	6	US-10-509-131-39	Sequence 39, Appl	c 383	10.4	74.3	781	6	US-10-953-349-24773	Sequence 24773, A
c 311	10.8	77.1	4074	7	US-11-217-529-4467	Sequence 4467, App	c 384	10.4	74.3	817	6	US-10-488-619-2102	Sequence 2102, App
c 312	10.8	77.1	4194	7	US-11-217-529-77339	Sequence 77339, A	c 385	10.4	74.3	837	6	US-10-953-349-18372	Sequence 18372, A
c 313	10.8	77.1	4337	7	US-11-293-697-1232	Sequence 1232, App	c 386	10.4	74.3	828	7	US-11-217-529-77579	Sequence 77579, A
c 314	10.8	77.1	4413	7	US-11-217-529-3933	Sequence 3933, App	c 387	10.4	74.3	830	6	US-10-953-349-39705	Sequence 39705, A
c 315	10.8	77.1	4894	6	US-10-511-937-566	Sequence 566, App	c 388	10.4	74.3	836	6	US-10-953-349-36674	Sequence 36674, A
c 316	10.8	77.1	5217	7	US-11-217-529-5142	Sequence 5142, App	c 389	10.4	74.3	873	6	US-10-953-349-21	Sequence 21, Appl
c 317	10.8	77.1	5223	7	US-11-217-529-5246	Sequence 5246, App	c 390	10.4	74.3	928	6	US-10-953-349-25780	Sequence 25780, A

c 391	10.4	74.3	951	7	US-11-217-529-975	Sequence 975, App	Sequence 975, App	464	10.4	74.3	1629	7	US-11-217-529-77846	Sequence 77846, A
c 392	10.4	74.3	951	7	US-11-217-529-2964	Sequence 2964, App	Sequence 2964, App	c 465	10.4	74.3	1641	7	US-11-217-529-78808	Sequence 78808, A
c 393	10.4	74.3	955	6	US-10-488-619-3026	Sequence 3026, App	Sequence 3026, App	c 466	10.4	74.3	1717	6	US-10-953-349-3286	Sequence 3286, A
c 394	10.4	74.3	960	7	US-11-217-529-1277	Sequence 1277, App	Sequence 1277, App	c 467	10.4	74.3	1727	6	US-10-511-937-457	Sequence 457, App
c 395	10.4	74.3	977	6	US-10-953-349-29094	Sequence 29094, A	Sequence 29094, A	c 468	10.4	74.3	1737	7	US-11-217-529-4822	Sequence 4822, App
c 396	10.4	74.3	1003	7	US-11-226-605-12	Sequence 12, Appl	Sequence 12, Appl	c 469	10.4	74.3	1763	7	US-11-293-697-2150	Sequence 2150, App
c 397	10.4	74.3	1003	7	US-11-226-605-58	Sequence 58, Appl	Sequence 58, Appl	c 470	10.4	74.3	1764	7	US-11-217-529-76317	Sequence 76317, A
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c 399	10.4	74.3	1014	6	US-10-953-349-19434	Sequence 19434, A	Sequence 19434, A	c 472	10.4	74.3	1829	6	US-10-953-349-7064	Sequence 7064, App
c 400	10.4	74.3	1022	6	US-10-953-349-36950	Sequence 36950, A	Sequence 36950, A	c 473	10.4	74.3	1838	7	US-10-953-697-1863	Sequence 1863, App
c 401	10.4	74.3	1032	7	US-11-217-529-3044	Sequence 3044, App	Sequence 3044, App	c 474	10.4	74.3	1846	7	US-11-293-697-2144	Sequence 2144, App
c 402	10.4	74.3	1039	6	US-10-953-349-27919	Sequence 27919, A	Sequence 27919, A	c 475	10.4	74.3	1848	6	US-10-519-335-5	Sequence 5, Appl
c 403	10.4	74.3	1059	7	US-11-217-529-7260	Sequence 7260, A	Sequence 7260, A	c 476	10.4	74.3	1861	6	US-10-953-349-7610	Sequence 7610, App
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c 405	10.4	74.3	1078	6	US-10-953-349-14448	Sequence 14448, A	Sequence 14448, A	c 478	10.4	74.3	1878	7	US-11-293-697-176	Sequence 176, App
c 406	10.4	74.3	1087	6	US-10-525-647-22	Sequence 22, Appl	Sequence 22, Appl	c 479	10.4	74.3	1878	6	US-10-519-335-3	Sequence 3, Appl
c 407	10.4	74.3	1101	6	US-10-953-349-36175	Sequence 36175, A	Sequence 36175, A	c 480	10.4	74.3	1878	7	US-11-293-697-2381	Sequence 2381, App
c 408	10.4	74.3	1105	6	US-10-953-349-16597	Sequence 16597, A	Sequence 16597, A	c 481	10.4	74.3	1881	7	US-11-217-529-5310	Sequence 5310, App
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c 412	10.4	74.3	1152	6	US-10-953-349-20671	Sequence 20671, A	Sequence 20671, A	c 485	10.4	74.3	1932	7	US-11-217-529-554	Sequence 554, App
c 413	10.4	74.3	1160	6	US-10-953-349-18848	Sequence 18848, A	Sequence 18848, A	c 486	10.4	74.3	1935	7	US-11-217-529-1137	Sequence 1137, App
c 414	10.4	74.3	1169	6	US-10-953-349-3649	Sequence 3649, App	Sequence 3649, App	c 487	10.4	74.3	1956	7	US-11-217-529-1907	Sequence 1907, App
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c 416	10.4	74.3	1185	6	US-10-953-349-29401	Sequence 29401, A	Sequence 29401, A	c 489	10.4	74.3	1959	6	US-10-953-349-35401	Sequence 35401, A
c 417	10.4	74.3	1209	7	US-11-217-529-77464	Sequence 77464, A	Sequence 77464, A	c 490	10.4	74.3	1992	7	US-11-217-529-5642	Sequence 5642, App
c 418	10.4	74.3	1212	7	US-11-217-529-370	Sequence 370, App	Sequence 370, App	c 491	10.4	74.3	1995	6	US-10-953-349-12090	Sequence 12090, A
c 419	10.4	74.3	1218	7	US-11-217-529-79983	Sequence 79983, A	Sequence 79983, A	c 492	10.4	74.3	2001	7	US-11-217-529-79229	Sequence 79229, A
c 420	10.4	74.3	1250	6	US-10-953-349-18920	Sequence 18920, A	Sequence 18920, A	c 493	10.4	74.3	2008	7	US-11-293-697-75	Sequence 75, Appl
c 421	10.4	74.3	1242	6	US-10-953-349-6692	Sequence 6692, App	Sequence 6692, App	c 494	10.4	74.3	2013	7	US-11-217-529-77566	Sequence 77566, A
c 422	10.4	74.3	1244	6	US-10-953-349-4128	Sequence 4128, App	Sequence 4128, App	c 495	10.4	74.3	2013	7	US-11-217-529-1571	Sequence 1571, App
c 423	10.4	74.3	1247	6	US-10-953-349-3580	Sequence 3580, App	Sequence 3580, App	c 496	10.4	74.3	2016	7	US-11-217-529-82328	Sequence 82328, A
c 424	10.4	74.3	1254	7	US-11-217-529-81314	Sequence 81314, A	Sequence 81314, A	c 497	10.4	74.3	2019	7	US-11-293-697-1629	Sequence 1629, App
c 425	10.4	74.3	1259	6	US-10-953-349-18783	Sequence 18783, A	Sequence 18783, A	c 498	10.4	74.3	2024	7	US-11-145-307A-55	Sequence 55, Appl
c 426	10.4	74.3	1275	7	US-11-421-154-102	Sequence 102, App	Sequence 102, App	c 499	10.4	74.3	2026	7	US-11-293-697-2111	Sequence 2111, App
c 427	10.4	74.3	1278	6	US-10-953-349-24527	Sequence 24527, A	Sequence 24527, A	c 500	10.4	74.3	2030	7	US-11-322-999-5	Sequence 5, Appl
c 428	10.4	74.3	1281	7	US-11-217-529-879	Sequence 879, App	Sequence 879, App	c 501	10.4	74.3	2030	7	US-11-217-529-5680	Sequence 5680, App
c 429	10.4	74.3	1282	6	US-10-953-349-29323	Sequence 29323, A	Sequence 29323, A	c 502	10.4	74.3	2051	6	US-10-953-349-7080	Sequence 7080, App
c 430	10.4	74.3	1323	6	US-10-505-928-380	Sequence 380, App	Sequence 380, App	c 503	10.4	74.3	2063	7	US-11-293-697-2390	Sequence 2390, App
c 431	10.4	74.3	1332	7	US-11-217-529-77527	Sequence 77527, A	Sequence 77527, A	c 504	10.4	74.3	2077	7	US-11-293-697-1908	Sequence 1908, App
c 432	10.4	74.3	1346	6	US-10-953-349-34301	Sequence 34301, A	Sequence 34301, A	c 505	10.4	74.3	2097	7	US-11-301-554-826	Sequence 826, App
c 433	10.4	74.3	1352	6	US-10-953-349-19492	Sequence 19492, A	Sequence 19492, A	c 506	10.4	74.3	2109	7	US-11-217-529-3350	Sequence 3350, App
c 434	10.4	74.3	1364	6	US-10-953-349-27423	Sequence 27423, A	Sequence 27423, A	c 507	10.4	74.3	2115	7	US-11-293-697-2250	Sequence 2250, App
c 435	10.4	74.3	1367	6	US-10-953-349-13239	Sequence 13239, A	Sequence 13239, A	c 508	10.4	74.3	2117	7	US-11-293-697-2421	Sequence 2421, App
c 436	10.4	74.3	1369	6	US-10-953-349-22871	Sequence 22871, A	Sequence 22871, A	c 509	10.4	74.3	2131	7	US-11-293-697-2421	Sequence 2421, App
c 437	10.4	74.3	1380	6	US-10-953-349-6755	Sequence 6755, App	Sequence 6755, App	c 510	10.4	74.3	2136	7	US-11-318-813-37	Sequence 37, Appl
c 438	10.4	74.3	1389	6	US-10-953-349-35006	Sequence 35006, A	Sequence 35006, A	c 511	10.4	74.3	2145	7	US-11-227-644-3	Sequence 3, Appl
c 439	10.4	74.3	1401	6	US-10-953-349-21919	Sequence 21919, A	Sequence 21919, A	c 512	10.4	74.3	2146	6	US-10-953-349-5657	Sequence 5657, App
c 440	10.4	74.3	1404	7	US-11-217-529-76780	Sequence 76780, A	Sequence 76780, A	c 513	10.4	74.3	2166	7	US-11-217-529-1236	Sequence 1236, App
c 441	10.4	74.3	1410	7	US-11-217-529-4030	Sequence 4030, App	Sequence 4030, App	c 514	10.4	74.3	2167	6	US-10-953-349-17117	Sequence 17117, A
c 442	10.4	74.3	1417	6	US-10-953-349-26201	Sequence 26201, A	Sequence 26201, A	c 515	10.4	74.3	2184	7	US-11-217-529-5288	Sequence 5288, App
c 443	10.4	74.3	1431	7	US-11-217-529-76683	Sequence 76683, A	Sequence 76683, A	c 516	10.4	74.3	2192	7	US-11-293-697-1340	Sequence 1340, App
c 444	10.4	74.3	1451	6	US-10-953-349-29115	Sequence 29115, A	Sequence 29115, A	c 517	10.4	74.3	2194	7	US-11-293-697-1951	Sequence 1951, App
c 445	10.4	74.3	1480	6	US-10-953-349-31871	Sequence 31871, A	Sequence 31871, A	c 518	10.4	74.3	2214	7	US-11-318-813-1	Sequence 1, Appl
c 446	10.4	74.3	1485	7	US-11-217-529-5036	Sequence 5036, App	Sequence 5036, App	c 519	10.4	74.3	2215	7	US-11-293-697-1751	Sequence 1751, App
c 447	10.4	74.3	1486	6	US-10-973-274-30	Sequence 30, Appl	Sequence 30, Appl	c 520	10.4	74.3	2235	6	US-11-293-697-935	Sequence 935, App
c 448	10.4	74.3	1500	7	US-11-293-697-1988	Sequence 1988, App	Sequence 1988, App	c 521	10.4	74.3	2250	6	US-10-953-349-7298	Sequence 7298, App
c 449	10.4	74.3	1542	7	US-11-217-529-77984	Sequence 77984, A	Sequence 77984, A	c 522	10.4	74.3	2265	7	US-11-217-529-76346	Sequence 76346, A
c 450	10.4	74.3	1553	7	US-11-248-986-25	Sequence 25, Appl	Sequence 25, Appl	c 523	10.4	74.3	2349	7	US-11-217-529-3488	Sequence 3488, App
c 451	10.4	74.3	1567	7	US-11-293-697-1059	Sequence 1059, App	Sequence 1059, App	c 524	10.4	74.3	2364	6	US-10-953-349-1490	Sequence 1490, App
c 452	10.4	74.3	1572	7	US-11-217-529-2215	Sequence 2215, App	Sequence 2215, App	c 525	10.4	74.3	2376	7	US-11-217-529-78788	Sequence 78788, A
c 453	10.4	74.3	1582	6	US-10-953-349-32115	Sequence 32115, A	Sequence 32115, A	c 526	10.4	74.3	2391	7	US-11-293-697-1862	Sequence 1862, App
c 454	10.4	74.3	1605	7	US-11-217-529-1809	Sequence 1809, App	Sequence 1809, App	c 527	10.4	74.3	2393	6	US-10-953-349-6275	Sequence 6275, App
c 455	10.4	74.3	1605	7	US-11-217-529-3550	Sequence 3550, App	Sequence 3550, App	c 528	10.4	74.3	2394	7	US-11-293-697-2296	Sequence 2296, App
c 456	10.4	74.3	1607	6	US-10-953-349-11722	Sequence 11722, A	Sequence 11722, A	c 529	10.4	74.3	2403	6	US-10-196-749-45	Sequence 45, Appl
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c 458	10.4	74.3	1617	7	US-11-217-529-4915	Sequence 4915, App	Sequence 4915, App	c 531	10.4	74.3	2408	7	US-11-293-697-225	Sequence 225, App
c 459	10.4	74.3	1618	6	US-10-953-349-13785	Sequence 13785, A	Sequence 13785, A	c 532	10.4	74.3	2421	7	US-11-217-529-4463	Sequence 4463, App
c 460	10.4	74.3	1618	6	US-10-953-349-29520	Sequence 29520, A	Sequence 29520, A	c 533	10.4	74.3	2455	7	US-11-293-697-411	Sequence 411, App
c 461	10.4	74.3	1619	7	US-11-301-554-801	Sequence 801, App	Sequence 801, App							

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538	10.4	74.3	2571	6	US-10-196-749-165	Sequence 165, App	c 611	10.4	74.3	14299	7	US-11-248-986-19	Sequence 19, Appl
539	10.4	74.3	2571	6	US-11-101-316-39	Sequence 39, Appl	c 612	10.4	74.3	50000	6	US-10-528-659-2	Sequence 2, Appl
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542	10.4	74.3	2625	7	US-11-217-529-3881	Sequence 3881, A	c 615	10.4	74.3	151830	6	US-10-519-335-37	Sequence 37, Appl
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544	10.4	74.3	2644	7	US-11-266-446-66	Sequence 66, Appl	c 617	10.4	74.3	25	7	US-11-217-529-20726	Sequence 20726, A
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546	10.4	74.3	2676	7	US-11-217-529-5102	Sequence 5102, App	c 619	10.4	74.3	25	7	US-11-217-529-31088	Sequence 31088, A
547	10.4	74.3	2688	7	US-11-293-697-2253	Sequence 2253, App	c 620	10.4	74.3	25	7	US-11-217-529-34939	Sequence 34939, A
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551	10.4	74.3	2760	7	US-11-302-678-63	Sequence 63, Appl	c 624	10.4	74.3	25	7	US-11-217-529-75267	Sequence 75267, A
552	10.4	74.3	2804	7	US-11-293-697-41	Sequence 41, Appl	c 625	10.4	74.3	25	7	US-11-217-529-98279	Sequence 98279, A
553	10.4	74.3	2816	7	US-11-293-697-206	Sequence 206, App	c 626	10.4	74.3	25	7	US-11-217-529-103808	Sequence 103808, A
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556	10.4	74.3	2931	7	US-11-217-529-3493	Sequence 3493, App	c 629	10.4	74.3	25	7	US-11-217-529-15792	Sequence 15792, A
557	10.4	74.3	2995	7	US-11-293-697-600	Sequence 600, App	c 630	10.4	74.3	25	7	US-11-217-529-158907	Sequence 158907, A
558	10.4	74.3	3023	7	US-11-293-697-665	Sequence 665, App	c 631	10.4	74.3	25	7	US-11-217-529-158909	Sequence 158909, A
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560	10.4	74.3	3081	7	US-11-293-697-872	Sequence 872, App	c 633	10.4	74.3	25	7	US-11-217-529-161356	Sequence 161356, A
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567	10.4	74.3	3210	7	US-11-217-529-1385	Sequence 1385, App	c 640	10.4	74.3	25	7	US-11-217-529-167107	Sequence 167107, A
568	10.4	74.3	3228	7	US-11-217-529-190982	Sequence 190982, A	c 641	10.4	74.3	51	7	US-11-245-248-1312	Sequence 1312, App
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571	10.4	74.3	3243	7	US-11-293-697-1332	Sequence 1332, App	c 644	10.4	74.3	294	7	US-11-219-563-137	Sequence 137, App
572	10.4	74.3	3246	7	US-11-293-697-1216	Sequence 1216, App	c 645	10.4	74.3	318	7	US-11-217-529-76269	Sequence 76269, A
573	10.4	74.3	3264	7	US-11-217-529-3050	Sequence 3050, App	c 646	10.4	74.3	321	7	US-11-217-529-166495	Sequence 166495, A
574	10.4	74.3	3276	7	US-11-217-529-2030	Sequence 2030, App	c 647	10.4	74.3	333	7	US-11-217-529-82142	Sequence 82142, A
575	10.4	74.3	3387	7	US-11-217-529-78908	Sequence 78908, A	c 648	10.4	74.3	355	7	US-11-301-554-749	Sequence 749, App
576	10.4	74.3	3420	7	US-11-217-529-71	Sequence 71, Appl	c 649	10.4	74.3	414	7	US-11-217-529-4286	Sequence 4286, App
577	10.4	74.3	3424	7	US-11-293-697-663	Sequence 663, App	c 650	10.4	74.3	434	7	US-11-301-554-1590	Sequence 1590, App
578	10.4	74.3	3547	7	US-11-293-697-1122	Sequence 1122, App	c 651	10.4	74.3	453	7	US-11-217-529-79980	Sequence 79980, A
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580	10.4	74.3	3660	7	US-11-217-529-2996	Sequence 2996, App	c 653	10.4	74.3	472	7	US-11-301-554-342	Sequence 342, App
581	10.4	74.3	3693	7	US-11-217-529-77316	Sequence 77316, A	c 654	10.4	74.3	476	6	US-10-953-349-14774	Sequence 14774, A
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585	10.4	74.3	3841	7	US-11-293-697-1374	Sequence 1374, App	c 658	10.4	74.3	510	7	US-11-217-529-2274	Sequence 2274, App
586	10.4	74.3	3873	7	US-11-217-529-77429	Sequence 77429, A	c 659	10.4	74.3	519	7	US-09-784-950-76	Sequence 76, Appl
587	10.4	74.3	3935	7	US-11-293-697-534	Sequence 534, App	c 660	10.4	74.3	541	6	US-10-981-300-3	Sequence 3, Appl
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589	10.4	74.3	4068	7	US-11-217-529-48	Sequence 48, Appl	c 662	10.4	74.3	548	6	US-10-488-619-2433	Sequence 2433, App
590	10.4	74.3	4122	6	US-10-505-928-427	Sequence 427, App	c 663	10.4	74.3	554	6	US-10-488-619-2433	Sequence 7, Appl
591	10.4	74.3	4246	6	US-10-505-928-544	Sequence 544, App	c 664	10.4	74.3	568	6	US-10-981-300-7	Sequence 1185, App
592	10.4	74.3	4314	6	US-10-511-937-553	Sequence 553, App	c 665	10.4	74.3	573	7	US-11-217-529-1185	Sequence 2347, App
593	10.4	74.3	4326	7	US-11-121-154-160	Sequence 160, App	c 666	10.4	74.3	577	6	US-10-488-619-2347	Sequence 1279, App
594	10.4	74.3	4498	7	US-11-217-529-190990	Sequence 190990, A	c 667	10.4	74.3	584	6	US-10-488-619-2623	Sequence 2623, App
595	10.4	74.3	4637	6	US-11-301-554-804	Sequence 804, App	c 668	10.4	74.3	597	7	US-11-217-529-2623	Sequence 2804, App
596	10.4	74.3	4791	6	US-10-505-928-647	Sequence 647, App	c 669	10.4	74.3	603	6	US-10-488-619-1989	Sequence 1989, App
597	10.4	74.3	5072	6	US-10-953-349-7998	Sequence 7998, App	c 670	10.4	74.3	626	6	US-10-488-619-1266	Sequence 1266, App
598	10.4	74.3	5310	6	US-11-217-529-77298	Sequence 77298, A	c 671	10.4	74.3	658	6	US-10-488-619-1266	Sequence 25980, A
599	10.4	74.3	5350	6	US-10-505-928-212	Sequence 212, App	c 672	10.4	74.3	673	6	US-10-953-349-37535	Sequence 37535, A
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601	10.4	74.3	6438	7	US-11-217-529-173840	Sequence 173840, A	c 674	10.4	74.3	717	7	US-11-217-529-244	Sequence 244, App
602	10.4	74.3	7463	6	US-10-953-349-38474	Sequence 38474, A	c 675	10.4	74.3	761	6	US-11-217-529-29793	Sequence 29793, A
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604	10.4	74.3	8764	7	US-11-322-999-137	Sequence 137, App	c 677	10.4	74.3	763	6	US-10-953-349-27599	Sequence 27599, A
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607	10.4	74.3	9973	6	US-10-857-260-29	Sequence 29, Appl	c 680	10.4	74.3	859	6	US-10-953-349-25851	Sequence 2, Appl
608	10.4	74.3	10211	6	US-10-505-928-326	Sequence 326, App	c 681	10.4	74.3	875	6	US-10-514-535-2	
609	10.4	74.3	10581	7	US-11-217-529-4304	Sequence 4304, App	c 682	10.4	74.3				

c 683	10	71.4	914	6	US-10-953-349-39424	Sequence 39424, A	c 756	10	71.4	1627	7	US-11-293-697-1835	Sequence 1835, Ap
c 684	10	71.4	930	7	US-11-217-529-4685	Sequence 4685, Ap	c 757	10	71.4	1628	7	US-11-293-697-1846	Sequence 1846, Ap
c 685	10	71.4	945	7	US-11-217-529-5482	Sequence 5482, Ap	c 758	10	71.4	1631	7	US-11-293-697-1630	Sequence 1630, Ap
c 686	10	71.4	960	7	US-11-217-529-82143	Sequence 82143, A	c 759	10	71.4	1633	7	US-11-293-697-1852	Sequence 1852, Ap
c 687	10	71.4	963	7	US-11-217-529-2815	Sequence 2815, Ap	c 760	10	71.4	1633	7	US-11-293-697-2197	Sequence 2197, Ap
c 688	10	71.4	990	7	US-11-217-529-6230	Sequence 6230, Ap	c 761	10	71.4	1639	7	US-11-293-697-2238	Sequence 2238, Ap
c 689	10	71.4	1026	7	US-11-219-563-135	Sequence 135, App	c 762	10	71.4	1701	7	US-11-106-762-10	Sequence 10, Appl
c 690	10	71.4	1094	6	US-10-953-349-35709	Sequence 35709, A	c 763	10	71.4	1704	7	US-11-217-529-77224	Sequence 77224, A
c 691	10	71.4	1095	7	US-11-217-529-82043	Sequence 82043, A	c 764	10	71.4	1725	6	US-10-953-349-27632	Sequence 27632, A
c 692	10	71.4	1107	7	US-11-217-529-78001	Sequence 78001, A	c 765	10	71.4	1731	7	US-11-244-678-5	Sequence 5, Appl
c 693	10	71.4	1108	6	US-10-953-349-411	Sequence 411, App	c 766	10	71.4	1750	6	US-10-953-349-10054	Sequence 10054, A
c 694	10	71.4	1119	7	US-11-217-529-76178	Sequence 76178, A	c 767	10	71.4	1759	7	US-11-293-697-2324	Sequence 2324, Ap
c 695	10	71.4	1129	6	US-10-953-349-18277	Sequence 18277, A	c 768	10	71.4	1763	7	US-11-293-697-1840	Sequence 1840, Ap
c 696	10	71.4	1132	6	US-10-953-349-3258	Sequence 3258, Ap	c 769	10	71.4	1767	6	US-10-953-349-22189	Sequence 22189, A
c 697	10	71.4	1151	6	US-10-953-349-35098	Sequence 35098, A	c 770	10	71.4	1775	6	US-10-953-349-32421	Sequence 32421, A
c 698	10	71.4	1152	6	US-10-953-349-28455	Sequence 28455, A	c 771	10	71.4	1790	7	US-11-293-697-2345	Sequence 2345, Ap
c 699	10	71.4	1156	6	US-10-953-349-11844	Sequence 11844, A	c 772	10	71.4	1802	7	US-11-293-697-2009	Sequence 2009, Ap
c 700	10	71.4	1166	6	US-10-953-349-28881	Sequence 28881, A	c 773	10	71.4	1805	6	US-10-953-349-12895	Sequence 12895, A
c 701	10	71.4	1213	7	US-11-244-678-6	Sequence 6, Appl	c 774	10	71.4	1815	7	US-11-217-529-75749	Sequence 75749, A
c 702	10	71.4	1227	6	US-10-953-349-27530	Sequence 27530, A	c 775	10	71.4	1820	7	US-11-244-678-3	Sequence 3, Appl
c 703	10	71.4	1248	7	US-11-217-529-39	Sequence 39, Appl	c 776	10	71.4	1821	7	US-11-293-697-1804	Sequence 1804, Ap
c 704	10	71.4	1251	7	US-11-217-529-248	Sequence 248, App	c 777	10	71.4	1822	7	US-11-293-697-130	Sequence 130, App
c 705	10	71.4	1255	6	US-10-953-349-11798	Sequence 11798, A	c 778	10	71.4	1828	7	US-11-244-678-1	Sequence 1, Appl
c 706	10	71.4	1290	7	US-11-302-678-54	Sequence 54, Appl	c 779	10	71.4	1837	7	US-11-293-697-1660	Sequence 1660, Ap
c 707	10	71.4	1307	6	US-10-953-349-27753	Sequence 27753, A	c 780	10	71.4	1837	7	US-11-293-697-1870	Sequence 1870, Ap
c 708	10	71.4	1312	6	US-10-953-349-21662	Sequence 21662, A	c 781	10	71.4	1842	7	US-11-217-529-1606	Sequence 1606, Ap
c 709	10	71.4	1330	6	US-10-981-300-19	Sequence 19, Appl	c 782	10	71.4	1857	7	US-11-217-529-2428	Sequence 2428, Ap
c 710	10	71.4	1330	6	US-10-953-349-14318	Sequence 14318, A	c 783	10	71.4	1871	6	US-10-196-749-301	Sequence 301, App
c 711	10	71.4	1344	6	US-10-713-648A-51	Sequence 51, Appl	c 784	10	71.4	1871	7	US-11-101-316-91	Sequence 91, Appl
c 712	10	71.4	1350	6	US-10-953-349-31595	Sequence 31595, A	c 785	10	71.4	1897	6	US-10-953-349-19352	Sequence 19352, A
c 713	10	71.4	1362	6	US-10-953-349-31213	Sequence 31213, A	c 786	10	71.4	1904	6	US-10-505-928-546	Sequence 546, App
c 714	10	71.4	1362	6	US-10-981-300-15	Sequence 15, Appl	c 787	10	71.4	1906	7	US-11-293-697-551	Sequence 551, App
c 715	10	71.4	1362	7	US-11-217-529-77394	Sequence 77394, A	c 788	10	71.4	1941	6	US-10-953-349-2086	Sequence 2086, Ap
c 716	10	71.4	1395	7	US-11-211-917-21	Sequence 21, Appl	c 789	10	71.4	1943	6	US-10-953-349-37312	Sequence 37312, A
c 717	10	71.4	1398	7	US-11-211-917-37	Sequence 37, Appl	c 790	10	71.4	2027	6	US-10-953-349-32588	Sequence 32588, A
c 718	10	71.4	1401	7	US-11-211-917-29	Sequence 29, Appl	c 791	10	71.4	2029	6	US-10-505-928-855	Sequence 855, App
c 719	10	71.4	1401	7	US-11-211-917-69	Sequence 69, Appl	c 792	10	71.4	2059	6	US-10-511-937-507	Sequence 507, App
c 720	10	71.4	1401	7	US-11-211-917-85	Sequence 85, Appl	c 793	10	71.4	2076	7	US-11-217-529-77476	Sequence 77476, A
c 721	10	71.4	1407	7	US-11-155-444-17	Sequence 17, Appl	c 794	10	71.4	2086	7	US-11-293-697-1875	Sequence 1875, Ap
c 722	10	71.4	1410	7	US-11-211-917-53	Sequence 53, Appl	c 795	10	71.4	2094	7	US-11-155-444-1	Sequence 1, Appl
c 723	10	71.4	1413	7	US-11-211-917-61	Sequence 61, Appl	c 796	10	71.4	2106	7	US-11-155-444-7	Sequence 7, Appl
c 724	10	71.4	1416	7	US-11-211-917-77	Sequence 77, Appl	c 797	10	71.4	2118	6	US-10-953-349-35155	Sequence 35155, A
c 725	10	71.4	1416	7	US-11-211-917-5	Sequence 5, Appl	c 798	10	71.4	2128	6	US-10-196-749-171	Sequence 171, App
c 726	10	71.4	1416	7	US-11-211-917-45	Sequence 45, Appl	c 799	10	71.4	2133	7	US-11-181-115-2	Sequence 2, Appl
c 727	10	71.4	1419	6	US-10-546-594-129	Sequence 129, App	c 800	10	71.4	2133	7	US-11-181-115-39	Sequence 39, Appl
c 728	10	71.4	1420	6	US-10-953-349-12396	Sequence 12396, A	c 801	10	71.4	2139	7	US-11-217-529-75693	Sequence 75693, A
c 729	10	71.4	1425	7	US-11-211-917-13	Sequence 13, Appl	c 802	10	71.4	2170	7	US-11-293-697-1753	Sequence 1753, Ap
c 730	10	71.4	1443	7	US-11-217-529-1848	Sequence 1848, Ap	c 803	10	71.4	2187	7	US-11-217-529-4382	Sequence 4382, Ap
c 731	10	71.4	1452	6	US-10-953-349-38070	Sequence 38070, A	c 804	10	71.4	2192	6	US-10-953-349-14231	Sequence 14231, A
c 732	10	71.4	1455	7	US-11-217-529-1502	Sequence 1502, Ap	c 805	10	71.4	2214	7	US-11-293-697-2000	Sequence 2000, Ap
c 733	10	71.4	1455	7	US-11-217-529-77427	Sequence 77427, A	c 806	10	71.4	2225	7	US-11-293-697-916	Sequence 916, App
c 734	10	71.4	1458	6	US-10-953-349-24219	Sequence 24219, A	c 807	10	71.4	2229	7	US-11-293-697-1081	Sequence 1081, Ap
c 735	10	71.4	1473	6	US-10-953-349-24770	Sequence 24770, A	c 808	10	71.4	2251	7	US-11-293-697-184	Sequence 184, App
c 736	10	71.4	1484	1	US-09-949-925-54	Sequence 54, Appl	c 809	10	71.4	2290	7	US-11-293-697-1793	Sequence 1793, Ap
c 737	10	71.4	1518	7	US-11-217-529-3186	Sequence 3186, Ap	c 810	10	71.4	2301	7	US-11-217-529-76159	Sequence 76159, A
c 738	10	71.4	1520	6	US-10-953-349-5515	Sequence 5515, Ap	c 811	10	71.4	2315	6	US-10-953-349-31228	Sequence 31228, A
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c 741	10	71.4	1566	7	US-11-293-697-1850	Sequence 1850, Ap	c 814	10	71.4	2430	7	US-11-217-529-1342	Sequence 1342, Ap
c 742	10	71.4	1575	6	US-10-953-349-21291	Sequence 21291, A	c 815	10	71.4	2476	7	US-11-293-697-110	Sequence 110, App
c 743	10	71.4	1578	7	US-11-219-563-131	Sequence 131, App	c 816	10	71.4	2530	7	US-11-066-633-1	Sequence 1, Appl
c 744	10	71.4	1590	6	US-10-505-928-838	Sequence 838, Appl	c 817	10	71.4	2574	7	US-11-293-697-2437	Sequence 2437, Ap
c 745	10	71.4	1590	7	US-11-106-014-43	Sequence 43, Appl	c 818	10	71.4	2623	7	US-11-293-697-1527	Sequence 1527, Ap
c 746	10	71.4	1602	7	US-11-293-697-1849	Sequence 1849, Ap	c 819	10	71.4	2627	7	US-11-293-697-1663	Sequence 1663, Ap
c 747	10	71.4	1605	7	US-11-293-697-1842	Sequence 1842, Ap	c 820	10	71.4	2752	7	US-11-293-697-2385	Sequence 2385, Ap
c 748	10	71.4	1612	7	US-11-293-697-1803	Sequence 1803, Ap	c 821	10	71.4	2769	6	US-10-953-349-11407	Sequence 11407, A
c 749	10	71.4	1613	7	US-11-293-697-1839	Sequence 1839, Ap	c 822	10	71.4	2770	7	US-11-293-697-1700	Sequence 1700, Ap
c 750	10	71.4	1613	7	US-11-293-697-1841	Sequence 1841, Ap	c 823	10	71.4	2795	7	US-11-293-697-1621	Sequence 1621, Ap
c 751	10	71.4	1613	7	US-11-293-697-1848	Sequence 1848, Ap	c 824	10	71.4	2840	6	US-10-953-349-34238	Sequence 34238, A
c 752	10	71.4	1618	7	US-11-293-697-1845	Sequence 1845, Ap	c 825	10	71.4	2859	7	US-11-293-697-1056	Sequence 1056, Ap
c 753	10	71.4	1620	7	US-11-293-697-1851	Sequence 1851, Ap	c 826	10	71.4	2898	7	US-11-217-529-1716	Sequence 1716, Ap
c 754	10	71.4	1622	7	US-11-293-697-1844	Sequence 1844, Ap	c 827	10	71.4	2952	7	US-11-293-697-1728	Sequence 1728, Ap
c 755	10	71.4	1624	7	US-11-293-697-1748	Sequence 1748, Ap	c 828	10	71.4	3047	6	US-10-953-349-11451	Sequence 11451, A

c 975 9.8 70.0 473 6 US-10-488-619-2659 Sequence 2659, Ap
c 976 9.8 70.0 480 6 US-10-488-619-2373 Sequence 2373, Ap
c 977 9.8 70.0 480 7 US-11-248-986-1 Sequence 1, Appl
c 978 9.8 70.0 483 6 US-10-488-619-298 Sequence 298, App
c 979 9.8 70.0 493 7 US-11-301-554-193 Sequence 193, App
c 980 9.8 70.0 495 7 US-11-217-529-79338 Sequence 79338, A
c 981 9.8 70.0 504 6 US-10-488-619-1248 Sequence 1248, Ap
c 982 9.8 70.0 507 7 US-11-217-529-4975 Sequence 4975, Ap
c 983 9.8 70.0 507 7 US-11-217-529-80087 Sequence 80087, A
c 984 9.8 70.0 525 7 US-11-217-529-80087 Sequence 80087, A
c 985 9.8 70.0 534 7 US-11-301-554-844 Sequence 844, App
c 986 9.8 70.0 534 7 US-11-217-529-81103 Sequence 81103, A
c 987 9.8 70.0 541 6 US-10-953-349-36788 Sequence 36788, A
c 988 9.8 70.0 546 7 US-11-301-554-129 Sequence 129, App
c 989 9.8 70.0 553 6 US-10-511-937-2808 Sequence 2808, Ap
c 990 9.8 70.0 559 6 US-10-473-173-341 Sequence 341, App
c 991 9.8 70.0 561 6 US-10-488-619-822 Sequence 822, App
c 992 9.8 70.0 568 6 US-10-488-619-1026 Sequence 1026, Ap
c 993 9.8 70.0 569 6 US-10-488-619-2716 Sequence 2716, Ap
c 994 9.8 70.0 570 6 US-10-473-173-19 Sequence 19, Appl
c 995 9.8 70.0 571 6 US-10-488-619-2657 Sequence 2657, Ap
c 996 9.8 70.0 574 6 US-10-488-619-2655 Sequence 2655, Ap
c 997 9.8 70.0 574 6 US-10-953-349-6017 Sequence 6017, Ap
c 998 9.8 70.0 576 6 US-10-488-619-2401 Sequence 2401, Ap
c 999 9.8 70.0 576 7 US-11-217-529-82432 Sequence 82432, A
1000 9.8 70.0 581 6 US-10-488-619-2947 Sequence 2947, Ap

ALIGNMENTS

RESULT 1
US-10-511-937-2635/c
; Sequence 2635, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2635
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2635
Query Match 88.6%; Score 12.4; DB 6; Length 50;
Best Local Similarity 92.9%; Pred. No. 28;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 19 GAAGGGTGTGCTTAC 6

RESULT 2

US-11-217-529-77707/c
; Sequence 77707, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77707
; LENGTH: 765
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77707
Query Match 88.6%; Score 12.4; DB 7; Length 765;
Best Local Similarity 92.9%; Pred. No. 48;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
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Db 335 GAAGTTGTGCTTAC 322

RESULT 3

US-10-953-349-20394
; Sequence 20394, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20394
; LENGTH: 1019
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20394
Query Match 88.6%; Score 12.4; DB 6; Length 1019;
Best Local Similarity 92.9%; Pred. No. 51;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTAC 14
|||||
Db 566 GAAGGTGTGCTTAC 579

RESULT 4

US-11-217-529-3002
; Sequence 3002, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3002
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3002

Query Match 88.6%; Score 12.4; DB 7; Length 1161;
Best Local Similarity 92.9%; Pred. No. 52;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
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Db 457 GAAGGTGCTTAC 470

RESULT 5

US-10-953-349-8649
; Sequence 8649, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8649
; LENGTH: 1304
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8649

Query Match 88.6%; Score 12.4; DB 6; Length 1304;
Best Local Similarity 92.9%; Pred. No. 53;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
|||||
Db 712 GAAGGTGCTTAC 725

RESULT 6

US-10-511-937-2804/c
; Sequence 2804, Application US/10511937
; Publication No. US20060088936A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2804
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2804

Query Match 88.6%; Score 12.4; DB 6; Length 1451;
Best Local Similarity 92.9%; Pred. No. 54;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
|||||
Db 1270 GAAGGTGCTTAC 1257

RESULT 7

US-11-217-529-82278
; Sequence 82278, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82278
; LENGTH: 2079
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82278

Query Match 88.6%; Score 12.4; DB 7; Length 2079;
Best Local Similarity 92.9%; Pred. No. 58;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTAC 14
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Db 489 GAAGGTGCTTAC 502

RESULT 8

US-10-953-349-4556/c
; Sequence 4556, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4556
; LENGTH: 3435
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4556

Query Match 88.6%; Score 12.4; DB 6; Length 3435;
Best Local Similarity 92.9%; Pred. No. 64;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 2396 GAAGGTGTGCTTCC 2383

RESULT 9

US-10-505-928-151/c

; Sequence 151, Application US/10505928

; Publication No. US2006008532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; PRIOR FILING DATE: 2004-08-27

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 151

; LENGTH: 128361

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-505-928-151

Query Match

Best Local Similarity 88.6%; Score 12.4; DB 6; Length 128361;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTAC 14

|||||

Db 55351 GAAGGTGGCTTAC 55338

RESULT 10

US-10-953-349-23971

; Sequence 23971, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 23971

; LENGTH: 650

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-23971

Query Match

Best Local Similarity 85.7%; Score 12; DB 6; Length 650;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12

|||||

Db 311 GAAGGTGTGCTT 322

RESULT 11

US-10-953-349-12654

; Sequence 12654, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 12654

; LENGTH: 651

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-12654

Query Match

Best Local Similarity 85.7%; Score 12; DB 6; Length 651;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12

|||||

Db 311 GAAGGTGTGCTT 322

RESULT 12

US-11-217-529-2897

; Sequence 2897, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUMIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 2897

; LENGTH: 951

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-2897

Query Match

Best Local Similarity 85.7%; Score 12; DB 7; Length 951;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTA 13

|||||

Db 719 AAGGTGTGCTTA 730

RESULT 13

US-10-953-349-17567

; Sequence 17567, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 17567

; LENGTH: 1212

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-17567

Query Match

Best Local Similarity 85.7%; Score 12; DB 6; Length 1212;

Best Local Similarity 100.0%; Pred. No. 93;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 109 GAAGGTGTGCTT 120

RESULT 14

US-11-024-544A-17/c
; Sequence 17, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-17

Query Match 85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 135 GAAGGTGTGCTT 124

RESULT 15

US-11-190-750-131/c
; Sequence 131, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 131
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-190-750-131

Query Match 85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 135 GAAGGTGTGCTT 124

RESULT 16

US-11-264-784-83/c
; Sequence 83, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-83

Query Match 85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
|||||
Db 135 GAAGGTGTGCTT 124

RESULT 17

US-11-264-737-124/c
; Sequence 124, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: DCOSEXHAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124

```
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (466)..(466)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-737-124

Query Match      85.7%; Score 12; DB 7; Length 1578;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
   |||||
Db 135 GAAGGTGTGCTT 124

RESULT 18
US-11-217-529-81407/c
; Sequence 81407, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81407
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81407

Query Match      85.7%; Score 12; DB 7; Length 1584;
Best Local Similarity 100.0%; Pred.No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTT 12
   |||||
Db 1154 GAAGGTGTGCTT 1143

RESULT 19
US-10-953-349-12369
; Sequence 12369, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12369
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
```

```
; NAME/KEY: misc feature
; LOCATION: (607)..(607)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (661)..(661)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (681)..(681)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (698)..(698)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (769)..(769)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (784)..(784)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (801)..(801)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (805)..(805)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (826)..(826)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (843)..(843)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (871)..(871)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (887)..(887)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (912)..(912)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (962)..(962)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (964)..(964)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (980)..(980)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1012)..(1012)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-12369
```

```
Query Match      85.7%; Score 12; DB 6; Length 1667;
Best Local Similarity 100.0%; Pred.No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GAAGGTGTGCTT 12
|||||
Db 1042 GAAGGTGTGCTT 1053

RESULT 20
US-11-024-544A-156/c
; Sequence 156, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 156
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)..(1093)
; OTHER INFORMATION: n is a, c, g, or t
US-11-024-544A-156

Query Match 85.7%; Score 12; DB 7; Length 1683;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTT 12
|||||
Db 367 GAAGGTGTGCTT 356

RESULT 21
US-11-190-750-127/c
; Sequence 127, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; TITLE OF INVENTION: OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127
; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Mortierella alpina
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1093)..(1093)
; OTHER INFORMATION: n is a, c, g, or t
US-11-190-750-127

Query Match 85.7%; Score 12; DB 7; Length 1683;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTT 12
|||||

Db 367 GAAGGTGTGCTT 356

RESULT 22
US-10-953-349-16812
; Sequence 16812, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16812
; LENGTH: 1749
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-16812

Query Match 85.7%; Score 12; DB 6; Length 1749;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGGTGTGCTT 12
|||||
Db 673 GAAGGTGTGCTT 684

RESULT 23
US-11-145-307A-163/c
; Sequence 163, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Acturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-163

Query Match 85.7%; Score 12; DB 7; Length 1841;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 AGGTGTGCTTAC 14
|||||
Db 1656 AGGTGTGCTTAC 1645

RESULT 24
US-11-217-529-2644/c
; Sequence 2644, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2644
; LENGTH: 3915
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (73)..(122)
; OTHER INFORMATION: a, c, g, t, unknown, or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1668)..(1721)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-2644

Query Match 85.7%; Score 12; DB 7; Length 3915;
Best Local Similarity 100.0%; Pred. No. 1.2e+02; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 1 GAAGGTGTGCTT 12
|||||

Db 1634 GAAGGTGTGCTT 1623

RESULT 25

US-11-024-544A-165/c
; Sequence 165, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 165
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMDGAT1-17
; NAME/KEY: misc.feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n is a, c, g, or t

Query Match 85.7%; Score 12; DB 7; Length 8666;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTT 12
|||||

Db 136 GAAGGTGTGCTT 125

RESULT 26

US-11-264-784-141/c
; Sequence 141, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:

; APPLICANT: E.I. duPont de Nemours & Co., Inc.

; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMDGAT1-17
; NAME/KEY: misc.feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n is a, c, g, or t

US-11-264-784-141

Query Match 85.7%; Score 12; DB 7; Length 8666;
Best Local Similarity 100.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

Qy 1 GAAGGTGTGCTT 12
|||||

Db 136 GAAGGTGTGCTT 125

RESULT 27

US-11-264-737-193/c
; Sequence 193, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn Qun
; TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 193
; LENGTH: 8666
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pMDGAT1-17
; NAME/KEY: misc.feature
; LOCATION: (467)..(467)
; OTHER INFORMATION: n is a, c, g, or t

Query Match

85.7%; Score 12; DB 7; Length 8666;

Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGGTGCTT 12
|||||
Db 136 GAAGGTGCTT 125

RESULT 28

US-11-217-529-21396/c
; Sequence 21396, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21396
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-21396

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
|||||
Db 22 AAGGGTGCTTAC 10

RESULT 29

US-11-217-529-21401/c
; Sequence 21401, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21401
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-21401

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
|||||

Db 19 AAGGGTGCTTAC 7

RESULT 30

US-11-217-529-68345
; Sequence 68345, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68345
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-68345

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGCTTAC 14
|||||
Db 8 AAGGTGCTTAC 20

RESULT 31

US-11-217-529-109203/c
; Sequence 109203, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 109203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-109203

Query Match 81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGCTTA 13
|||||
Db 13 GAAGGTGCTTA 1

RESULT 32

US-11-217-529-134611/c

```
/ Sequence 134611, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 134611
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-134611

Query Match      81.4%; Score 11.4; DB 7; Length 25;
Best Local Similarity 92.3%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      21 AAGGTGTGCATAC 9
|||||

RESULT 33
US-11-217-529-1402/c
/ Sequence 1402, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1402
/ LENGTH: 357
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-1402

Query Match      81.4%; Score 11.4; DB 7; Length 357;
Best Local Similarity 92.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      101 AAGGGGTGCTTAC 89
|||||

RESULT 34
US-11-217-529-5611
/ Sequence 5611, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
```

```
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5611
/ LENGTH: 393
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-5611

Query Match      81.4%; Score 11.4; DB 7; Length 393;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      155 AAGGTGTGCATAC 167
|||||

RESULT 35
US-11-217-529-79973/c
/ Sequence 79973, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 79973
/ LENGTH: 429
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-79973

Query Match      81.4%; Score 11.4; DB 7; Length 429;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAGGTGTGCTTAC 14
Db      290 AAGGTGTGCATAC 278
|||||

RESULT 36
US-10-488-619-1258/c
/ Sequence 1258, Application US/10488619
/ Publication No. US20060099578A1
/ GENERAL INFORMATION:
/ APPLICANT: Greenlee, Winner and Sullivan, P.C.
/ TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
/ TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
/ FILE REFERENCE: 98-01 WO
/ CURRENT APPLICATION NUMBER: US/10/488,619
/ CURRENT FILING DATE: 2004-03-01
/ NUMBER OF SEQ ID NOS: 3040
```


; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1258
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1258

Query Match 81.4%; Score 11.4; DB 6; Length 436;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||
Db 115 GAGGGTGTGCTTA 103

RESULT 37

US-10-488-619-102/c
; Sequence 102, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(442)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-102

Query Match 81.4%; Score 11.4; DB 6; Length 442;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||
Db 74 GAAGGTGTGCATA 62

RESULT 38

US-10-488-619-215/c
; Sequence 215, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 215
; LENGTH: 491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-215

Query Match 81.4%; Score 11.4; DB 6; Length 491;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||

Db 426 GAAGGTGAGCTTA 414

RESULT 39

US-10-488-619-637/c
; Sequence 637, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 637
; LENGTH: 513
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-637

Query Match 81.4%; Score 11.4; DB 6; Length 513;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
||| ||||| |||||
Db 472 AAAGTGTGCTTAC 460

RESULT 40

US-10-488-619-214
; Sequence 214, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-214

Query Match 81.4%; Score 11.4; DB 6; Length 517;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
||| ||||| |||||
Db 94 GAAGGTGAGCTTA 106

RESULT 41

US-10-953-349-6188/c
; Sequence 6188, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6188

```
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6188

Query Match      81.4%; Score 11.4; DB 6; Length 538;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
Db 351 GAAGTTGTGCTTA 339

RESULT 42
US-10-488-619-636
; Sequence 636, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 636
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-636

Query Match      81.4%; Score 11.4; DB 6; Length 545;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGGTGTGCTTAC 14
Db 136 AAGTGTGCTTAC 148

RESULT 43
US-10-488-619-202
; Sequence 202, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-202

Query Match      81.4%; Score 11.4; DB 6; Length 547;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
Db 109 GAAGGTGAGCTTA 121

RESULT 44
US-10-488-619-2061
; Sequence 2061, Application US/10488619
```

```
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2061
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2061

Query Match      81.4%; Score 11.4; DB 6; Length 561;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGGTGTGCTTAC 14
Db 190 AAGCTGTGCTTAC 202

RESULT 45
US-10-488-619-1924/c
; Sequence 1924, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1924
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1924

Query Match      81.4%; Score 11.4; DB 6; Length 592;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAGGTGTGCTTA 13
Db 531 GAAGGAGTGCTTA 519

RESULT 46
US-11-217-529-2
; Sequence 2, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHKAEI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
```

```
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Saccharomyces sp.
US-11-217-529-2

Query Match      81.4%; Score 11.4; DB 7; Length 609;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
   |||||
Db 451 GAAGGTGTGATTA 463

RESULT 47
US-11-217-529-1593
; Sequence 1593, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SONTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1593
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1593

Query Match      81.4%; Score 11.4; DB 7; Length 609;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
   |||||
Db 451 GAAGGTGTGATTA 463

RESULT 48
US-10-488-619-2060/c
; Sequence 2060, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2060
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2060

Query Match      81.4%; Score 11.4; DB 6; Length 668;
Best Local Similarity 92.3%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
   ||| |||||
```

```
Db 505 AAGCTGTGCTTAC 493

RESULT 49
US-10-488-619-1923
; Sequence 1923, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1923
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1923

Query Match      81.4%; Score 11.4; DB 6; Length 711;
Best Local Similarity 92.3%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGGTGTGCTTA 13
   |||||
Db 170 GAAGGAGTGCTTA 182

RESULT 50
US-11-249-111-37/c
; Sequence 37, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Lubbers, Mark W
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; FILE REFERENCE: 13353.1048ulc2
; CURRENT APPLICATION NUMBER: US/11/249,111
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Lactobacillus rhamnosus
US-11-249-111-37

Query Match      81.4%; Score 11.4; DB 7; Length 840;
Best Local Similarity 92.3%; Pred. No. 2e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AAGGTGTGCTTAC 14
   |||||
Db 632 AAGGTGTCTTAC 620

Search completed: May 31, 2006, 22:07:44
Job time : 67 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 46.9259 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21
Sequence: 1 tttctttttctctattaatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SID33/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SID33/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SID33/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SID33/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SID33/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SID33/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SID33/ptodata/2/ina/PCUTUS COMB.seq:*
- 8: /EMC_Celerra_SID33/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SID33/ptodata/2/ina/RG COMB.seq:*
- 10: /EMC_Celerra_SID33/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	21	100.0	36	3	US-09-109-329-14
C 2	21	100.0	36	3	US-09-109-329-15
C 3	21	100.0	59	3	US-09-109-329-3
C 4	21	100.0	89	3	US-09-109-329-4
C 5	21	100.0	108	3	US-09-109-329-13
C 6	21	100.0	2007	2	US-08-743-637B-169
C 7	21	100.0	2007	3	US-08-526-840B-169
C 8	21	100.0	2028	3	US-09-134-001C-1710
C 9	19.4	92.4	781	4	US-09-297-648-4022
C 10	19.4	92.4	6254	3	US-08-956-171E-404
C 11	19.4	92.4	6254	3	US-08-781-986A-404
C 12	19.4	92.4	23174	3	US-09-949-016-14387
C 13	19.4	92.4	23187	3	US-09-949-016-12235
C 14	18.4	87.6	459	3	US-09-328-352-1787
C 15	18.4	87.6	589	3	US-09-949-016-182944
C 16	18.4	87.6	601	3	US-09-949-016-182941
C 17	18.4	87.6	601	3	US-09-949-016-182942
C 18	18.4	87.6	601	3	US-09-949-016-182943
C 19	18.4	87.6	3650	3	US-09-710-279-3756
C 20	18.4	87.6	41737	3	US-09-949-016-12204
C 21	18.4	87.6	41741	3	US-09-949-016-16983
C 22	18.4	87.6	80269	3	US-09-949-016-15681
C 23	18.4	87.6	385136	3	US-09-949-016-16073

24	17.8	84.8	192	3	US-09-248-796A-9636	Sequence 9636, Ap
25	17.8	84.8	503	3	US-09-621-976-2887	Sequence 2887, Ap
C 26	17.8	84.8	1341	3	US-09-830-230A-572	Sequence 572, App
27	17.8	84.8	1350	7	US-08-244-205-1	Sequence 1, Appli
28	17.8	84.8	1350	7	PCT-US92-10284-1	Sequence 1, Appli
C 29	17.8	84.8	1410	3	US-09-830-230A-571	Sequence 21, App
C 30	17.8	84.8	1761	3	US-09-369-247-21	Sequence 21, Appl
C 31	17.8	84.8	1761	3	US-10-062-548-21	Sequence 21, Appl
C 32	17.8	84.8	114139	3	US-09-949-016-16536	Sequence 16536, A
C 33	17.8	84.8	173992	3	US-09-949-016-13379	Sequence 13379, A
C 34	17.8	84.8	174170	3	US-09-949-016-14810	Sequence 14810, A
C 35	17.8	84.8	174170	3	US-09-949-016-14811	Sequence 14811, A
C 36	17.8	84.8	174318	3	US-09-949-016-11880	Sequence 11880, A
C 37	17.8	84.8	174318	3	US-09-949-016-14812	Sequence 14812, A
C 38	17.8	84.8	174318	3	US-09-949-016-14813	Sequence 14813, A
C 39	17.8	84.8	256287	3	US-09-949-016-14608	Sequence 14608, A
C 40	17.8	84.8	321022	3	US-09-949-016-11852	Sequence 11852, A
C 41	17.8	84.8	321022	3	US-09-949-016-14166	Sequence 14166, A
C 42	17.4	82.9	232	3	US-09-621-976-17701	Sequence 17701, A
C 43	17.4	82.9	450	3	US-09-621-976-15099	Sequence 15099, A
C 44	17.4	82.9	601	3	US-09-949-016-27126	Sequence 27126, A
C 45	17.4	82.9	601	3	US-09-949-016-45118	Sequence 45118, A

ALIGNMENTS

RESULT 1
US-09-109-329-14/c
; Sequence 14, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-14

Query Match 100.0%; Score 21; DB 3; Length 36;
Best Local Similarity 100.0%; Pred.No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
|||||
DB 24 TTTCTTTTCTCTATTATG 4

RESULT 2
US-09-109-329-15/c
; Sequence 15, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-15

Query Match      100.0%; Score 21; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 24 TTTTCTTTTCTCTATTAAATG 4

RESULT 3
US-09-109-329-3/c
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-3

Query Match      100.0%; Score 21; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 29 TTTTCTTTTCTCTATTAAATG 9

RESULT 4
US-09-109-329-4
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
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; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match      100.0%; Score 21; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 43 TTTTCTTTTCTCTATTAAATG 63

RESULT 5
US-09-109-329-13/c
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-13

Query Match      100.0%; Score 21; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTCTATTAAATG 21
Db 49 TTTTCTTTTCTCTATTAAATG 29

RESULT 6
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/743,637B
FILING DATE: 04-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,840
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match 100.0%; Score 21; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
|||||
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 7
US-08-526-840B-169/c
Sequence 169, Application US/08526840B
Patent No. 6001564
GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
NUMBER OF SEQUENCES: 177
CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202-4497

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,840B
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/304,732
FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 21; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
|||||
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 8
US-09-134-001C-1710/c
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 21; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
|||||
Db 976 TTTTCTTTTCTCTATTAAATG 956

RESULT 9
US-09-297-648-4022/c
Sequence 4022, Application US/09297648
Patent No. 6964868
GENERAL INFORMATION:
APPLICANT: Williams, Lewis T.
APPLICANT: Escobedo, Jaime
APPLICANT: Innis, Michael A.
APPLICANT: Garcia, Pablo Dominguez
APPLICANT: Sudduth-Klinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Randazzo, Filippo
APPLICANT: Giese, Klaus
APPLICANT: Kennedy, Giulia C.
APPLICANT: Pot, David
APPLICANT: Kassan, Altaf
APPLICANT: Lamson, George
APPLICANT: Drmanac, Radoje
APPLICANT: Crkvenjakov, Radomir
APPLICANT: Dickson, Mark
APPLICANT: Drmanac, Snezana
APPLICANT: Labat, Ivan
APPLICANT: Leshkowitz, Dena

APPLICANT: Kita, David
APPLICANT: Garcia, Veronica
APPLICANT: Jones, William Lee
APPLICANT: Stache-Crain, Biljit
TITLE OF INVENTION: No. 6964868el Human Genes and Gene Expression
TITLE OF INVENTION: Products II

FILE REFERENCE: 2300-1481
CURRENT APPLICATION NUMBER: US/09/297,648

CURRENT FILING DATE: 2000-03-10

PRIOR APPLICATION NUMBER: 60/072,910

PRIOR FILING DATE: 1998-01-28

PRIOR APPLICATION NUMBER: 60/075,954

PRIOR FILING DATE: 1998-02-24

PRIOR APPLICATION NUMBER: 60/080,666

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: 60/080,515

PRIOR FILING DATE: 1998-04-03

PRIOR APPLICATION NUMBER: 60/080,114

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/105,234

PRIOR FILING DATE: 1998-10-21

NUMBER OF SEQ ID NOS: 5252

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4022

LENGTH: 781

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(781)

OTHER INFORMATION: n = A,T,C or G

US-09-297-648-4022

Query Match 92.4%; Score 19.4; DB 4; Length 781;
Best Local Similarity 95.2%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21
||||| ||||| ||||| ||||| |||||
Db 474 TTTTCATTCTCTATTATG 454

RESULT 10

US-08-956-171E-404/c

Sequence 404, Application US/08956171E

Patent No. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 404:

SEQUENCE CHARACTERISTICS:

LENGTH: 6254 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 404:

US-08-956-171E-404

Query Match 92.4%; Score 19.4; DB 3; Length 6254;

Best Local Similarity 95.2%; Pred. No. 2.3e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21

||||| ||||| ||||| ||||| |||||

Db 2565 TTTTCTTTTCTCTATCAATG 2545

RESULT 11

US-08-781-986A-404/c

Sequence 404, Application US/08781986A

Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 404:

SEQUENCE CHARACTERISTICS:

LENGTH: 6254 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986A-404

Query Match 92.4%; Score 19.4; DB 3; Length 6254;

Best Local Similarity 95.2%; Pred. No. 2.3e+02;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAG 21
|||||
Db 2565 TTTTCTTTTCTCTATTAAAG 2545

RESULT 12
US-09-949-016-14387
; Sequence 14387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14387
; LENGTH: 23174
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14387

Query Match 92.4%; Score 19.4; DB 3; Length 23174;
Best Local Similarity 95.2%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAG 21
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Db 6412 TTTTCTTTTCTCTATTAAAG 6432

RESULT 13
US-09-949-016-12235
; Sequence 12235, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12235
; LENGTH: 23187
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12235

Query Match 92.4%; Score 19.4; DB 3; Length 23187;
Best Local Similarity 95.2%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAG 21
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Db 6427 TTTTCTTTTCTCTATTAAAG 6447

RESULT 14
US-09-328-352-1787/c
; Sequence 1787, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1787
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1787

Query Match 87.6%; Score 18.4; DB 3; Length 459;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
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Db 419 TTTTCTTTTCTCTATTAAAT 400

RESULT 15

US-09-949-016-182944/c
; Sequence 182944, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182944
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-182944

Query Match 87.6%; Score 18.4; DB 3; Length 589;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTTTCTTTTCTCTATTAAATG 21
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Db 549 TTTTCTTTTCTCTATTAAATG 530

Search completed: May 31, 2006, 21:13:02
Job time : 48.9259 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 545.568 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-20
Perfect score: 21
Sequence: 1 ttttcttttctcttaatag 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	3	US-09-865-579A-10
2	21	100.0	21	3	US-09-865-579A-20
3	21	100.0	39	3	US-09-865-579A-27
4	21	100.0	1957	9	US-10-479-674-82
5	21	100.0	2007	3	US-09-452-599-169
6	21	100.0	2007	7	US-10-121-120-169
7	21	100.0	2007	9	US-10-479-674-78
8	21	100.0	2007	9	US-10-479-674-91
9	21	100.0	2007	9	US-10-121-120-169
10	21	100.0	2028	8	US-10-724-972A-3141
11	19.4	92.4	699	3	US-09-815-242-4505
12	19.4	92.4	699	3	US-09-815-242-4505
13	19.4	92.4	699	3	US-09-815-242-4505
14	19.4	92.4	699	8	US-10-282-122A-7879
15	19.4	92.4	781	10	US-10-779-543-4866
16	19.4	92.4	6254	2	US-08-781-986A-404
17	19.4	92.4	6254	8	US-10-329-624-404

18	19	90.5	623	6	US-10-027-632-113610	Sequence 113610,
19	19	90.5	623	6	US-10-027-632-113611	Sequence 113611,
20	19	90.5	623	7	US-10-027-632-113610	Sequence 113610,
21	19	90.5	623	7	US-10-027-632-113611	Sequence 113611,
22	19	90.5	1203	4	US-09-925-065A-88445	Sequence 88445, A
23	19	90.5	1203	5	US-09-925-065A-88445	Sequence 88445, A
24	19	90.5	1203	12	US-10-301-480-189686	Sequence 189686,
25	19	90.5	1203	12	US-10-301-480-803095	Sequence 803095,
26	18.4	87.6	43	9	US-10-741-849-101	Sequence 101, App
27	18.4	87.6	170	8	US-10-424-599-22484	Sequence 22484, A
28	18.4	87.6	369	5	US-09-925-065A-261289	Sequence 261289,
29	18.4	87.6	369	5	US-09-925-065A-261289	Sequence 261289,
30	18.4	87.6	453	8	US-10-282-122A-8499	Sequence 8499, Ap
31	18.4	87.6	530	9	US-10-357-930-52735	Sequence 52735, A
32	18.4	87.6	623	4	US-09-925-065A-534873	Sequence 534873,
33	18.4	87.6	623	5	US-09-925-065A-534873	Sequence 534873,
34	18.4	87.6	762	4	US-09-925-065A-714264	Sequence 714264,
35	18.4	87.6	762	5	US-09-925-065A-714264	Sequence 714264,
36	18.4	87.6	978	7	US-10-369-493-40382	Sequence 40382, A
37	18.4	87.6	1999	10	US-10-481-032A-797	Sequence 797, App
38	18.4	87.6	2000	3	US-09-938-842A-4244	Sequence 4244, Ap
39	18.4	87.6	2000	3	US-09-938-842A-4244	Sequence 4244, Ap
40	18.4	87.6	2198	10	US-10-481-032A-698	Sequence 698, App
41	18.4	87.6	2395	10	US-10-750-185-26666	Sequence 26666, A
42	18.4	87.6	2395	10	US-10-750-185-26666	Sequence 26666, A
43	18.4	87.6	3650	10	US-10-793-626-3756	Sequence 3756, Ap
44	18.4	87.6	274869	9	US-10-741-600-17650	Sequence 17650, A
45	18.4	87.6	301692	7	US-10-428-487-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-09-865-579A-10
; Sequence 10, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Saicho, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; FILE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 958-003-27
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-10

Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTTAATG 21

DB 1 TTTTCTTTTCTCTTAATG 21

RESULT 2

US-09-865-579A-20
; Sequence 20, Application US/09865579A

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; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saico, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-20

Query Match          100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 1 TTTTCTTTTCTCTATTAAATG 21

RESULT 3
US-09-865-579A-27
; Sequence 27, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saico, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-27

Query Match          100.0%; Score 21; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 1 TTTTCTTTTCTCTATTAAATG 21

RESULT 4
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
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; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Roesbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match          100.0%; Score 21; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 905 TTTTCTTTTCTCTATTAAATG 885

RESULT 5
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match          100.0%; Score 21; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 6
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
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; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 21; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 7
US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 8
US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match      100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
   |||||||
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 9
US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match      100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 10
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
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US-10-121-120-169
Query Match          100.0%; Score 21; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||
Db 955 TTTTCTTTTCTCTATTAAATG 935

RESULT 11
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match          100.0%; Score 21; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 976 TTTTCTTTTCTCTATTAAATG 956

RESULT 12
US-09-815-242-4505/c
; Sequence 4505, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8471
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(699)
US-09-815-242-8471

Query Match          92.4%; Score 19.4; DB 3; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||
Db 491 TTTTCTTTTCTCTATTAAATG 471

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; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4505
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-4505

Query Match          92.4%; Score 19.4; DB 3; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||
Db 491 TTTTCTTTTCTCTATTAAATG 471

RESULT 13
US-09-815-242-8471/c
; Sequence 8471, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8471
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(699)
US-09-815-242-8471

Query Match          92.4%; Score 19.4; DB 3; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
    |||||
Db 491 TTTTCTTTTCTCTATTAAATG 471

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RESULT 14

US-10-282-122A-7879/c
; Sequence 7879, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/131,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7879
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-7879

Query Match 92.4%; Score 19.4; DB 8; Length 699;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
|||||
Db 491 TTTCTTTTCTCTATCAATG 471

RESULT 15

US-10-779-543-4866/c
; Sequence 4866, Application US/10779543
; Publication No. US20050227917A1
; GENERAL INFORMATION:
; APPLICANT: Williams et al
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-21302
; CURRENT APPLICATION NUMBER: US/10/779,543
; CURRENT FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 10/076,555

; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 09/217,471
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/068,755
; PRIOR FILING DATE: 1997-12-23
; PRIOR APPLICATION NUMBER: 60/080,664
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: 60/105,234
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 09/297,648
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: PCT/US99/01619
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: 60/072,910
; PRIOR FILING DATE: 1998-01-28
; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4866
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4, 5, 6, 7, 11, 13, 19, 584, 610, 690, 756
; OTHER INFORMATION: n = A,T,C or G
US-10-779-543-4866

Query Match 92.4%; Score 19.4; DB 10; Length 781;
Best Local Similarity 95.2%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTATTATG 21
|||||
Db 474 TTTCTTTTCTCTATTATG 454

Search completed: May 31, 2006, 23:02:17
Job time : 546.568 secs

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 8.03704 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-20

Perfect score: 21

Sequence: 1 ttttcttttctctattaatg 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 5886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.4	87.6	1433	6	US-10-953-349-12899 Sequence 12899, A
C 2	17.8	84.8	3118	7	US-11-293-697-386 Sequence 386, App
C 3	16.8	80.0	449	6	US-10-488-619-1987 Sequence 1987, App
C 4	16.8	80.0	1039	6	US-10-953-349-22805 Sequence 22805, A
C 5	16.8	80.0	2628	7	US-11-264-784-50 Sequence 50, Appl
C 6	16.8	80.0	2628	7	US-11-264-737-83 Sequence 83, Appl
C 7	16.4	78.1	1340	6	US-10-953-349-26656 Sequence 26656, A
C 8	16.2	77.1	876	6	US-10-953-349-10770 Sequence 10770, A
C 9	16.2	77.1	1379	6	US-10-511-937-506 Sequence 506, App
C 10	16.2	77.1	1429	6	US-10-953-349-4335 Sequence 4335, App
C 11	16.2	77.1	1508	6	US-10-953-349-9239 Sequence 9239, App
C 12	16.2	77.1	1848	6	US-10-524-648-25 Sequence 25, Appl
C 13	16.2	77.1	1973	6	US-10-953-349-8854 Sequence 8854, App
C 14	16.2	77.1	2082	6	US-10-953-349-22034 Sequence 22034, A
C 15	16.2	77.1	2864	6	US-10-370-953-139 Sequence 139, App
C 16	16.2	77.1	3059	7	US-11-246-999-19 Sequence 19, Appl
C 17	16.2	77.1	3069	7	US-11-312-958-49 Sequence 49, Appl
C 18	16.2	77.1	3516	7	US-11-217-528-1696 Sequence 1696, App
C 19	15.8	75.2	333	7	US-11-217-529-79539 Sequence 79539, A
C 20	15.8	75.2	602	7	US-11-301-554-1564 Sequence 1564, App
C 21	15.8	75.2	967	6	US-10-953-349-25612 Sequence 25612, A
C 22	15.8	75.2	2370	7	US-11-293-697-1032 Sequence 1032, App
C 23	15.8	75.2	3231	7	US-11-217-529-76288 Sequence 76288, A
C 24	15.8	75.2	4015	7	US-11-293-697-627 Sequence 627, App
C 25	15.8	75.2	4465	6	US-10-505-928-528 Sequence 528, App

C 26	15.8	75.2	4465	6	US-10-511-937-460 Sequence 460, App
C 27	15.8	75.2	4856	6	US-10-505-928-242 Sequence 242, App
C 28	15.8	75.2	70865	6	US-10-505-928-596 Sequence 596, App
C 29	15.4	73.3	366	7	US-11-217-529-80588 Sequence 80588, A
C 30	15.4	73.3	908	6	US-10-953-349-762 Sequence 762, App
C 31	15.4	73.3	1434	6	US-10-953-349-24368 Sequence 24368, A
C 32	15.4	73.3	1960	7	US-11-293-697-1665 Sequence 1665, App
C 33	15.4	73.3	2565	6	US-10-953-349-8347 Sequence 8347, App
C 34	15.4	73.3	2787	7	US-11-293-697-1524 Sequence 1524, App
C 35	15.4	73.3	2991	7	US-11-217-529-5421 Sequence 5421, App
C 36	15.4	73.3	37426	6	US-10-473-173-32 Sequence 17, Appl
C 37	15.4	73.3	42999	7	US-11-284-877-17 Sequence 17, Appl
C 38	15.2	72.4	156	7	US-11-217-529-80094 Sequence 80094, A
C 39	15.2	72.4	261	6	US-10-473-173-430 Sequence 430, App
C 40	15.2	72.4	342	7	US-11-217-529-191052 Sequence 191052, A
C 41	15.2	72.4	390	7	US-11-217-529-78848 Sequence 78848, A
C 42	15.2	72.4	406	7	US-11-301-554-1150 Sequence 1150, App
C 43	15.2	72.4	546	7	US-11-217-529-79406 Sequence 79406, A
C 44	15.2	72.4	651	6	US-10-953-349-28191 Sequence 28191, A
C 45	15.2	72.4	653	6	US-10-953-349-14981 Sequence 14981, A

ALIGNMENTS

RESULT 1

US-10-953-349-12899/c
; Sequence 12899, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12899
; LENGTH: 1433
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-12899

Query Match 87.6%; Score 18.4; DB 6; Length 1433;
Best Local Similarity 95.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	TTTTCTTTTCTCTATTAT 20
Db	23	TTTTCTTTTCTCTATTAT 4

RESULT 2

US-11-293-697-386
; Sequence 386, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 386
; LENGTH: 3118
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-386

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Query Match      84.8%; Score 17.8; DB 7; Length 3118;
Best Local Similarity 90.5%; Pred. No. 77;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
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Db 2998 TTTTCTGTGTGCTATTAAATG 3018

RESULT 3
US-10-488-619-1987
; Sequence 1987, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1987
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1987

Query Match      80.0%; Score 16.8; DB 6; Length 449;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
    ||||| ||||| ||||| |||||
Db 10 TTTTCTTTTCTCTTTTAAAT 29

RESULT 4
US-10-953-349-22805
; Sequence 22805, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22805
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22805

Query Match      80.0%; Score 16.8; DB 6; Length 1039;
Best Local Similarity 90.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
    ||||| ||||| ||||| |||||
Db 1002 TTTTATTTTGTCTATTAAAT 1021

RESULT 5
US-11-264-784-50/c
; Sequence 50, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
```

```
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 50
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Rattus norvegicus (GenBank Accession No. AB071986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(893)
; OTHER INFORMATION: C16/18 elongase
US-11-264-784-50

Query Match      80.0%; Score 16.8; DB 7; Length 2628;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
    ||||| ||||| ||||| |||||
Db 957 TTTTCTTTTGTCTATTATT 938

RESULT 6
US-11-264-737-83/c
; Sequence 83, Application US/11264737
; Publication No. US20060110806A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter J.
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Ragghianti, James John
; APPLICANT: Seip, John E.
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn Qun
; TITLE OF INVENTION: DOCOSAHEXAENOIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3160 US NA
; CURRENT APPLICATION NUMBER: US/11/264,737
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 2628
; TYPE: DNA
; ORGANISM: Rattus norvegicus (GenBank Accession No. AB071986)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(893)
; OTHER INFORMATION: C16/18 elongase
US-11-264-737-83

Query Match      80.0%; Score 16.8; DB 7; Length 2628;
Best Local Similarity 90.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAAT 20
    ||||| ||||| ||||| |||||
Db 957 TTTTCTTTTGTCTATTATT 938
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RESULT 7
US-10-953-349-26656/c
; Sequence 26656, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26656
; LENGTH: 1540
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-26656

Query Match      78.1%; Score 16.4; DB 6; Length 1540;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATTA 18
Db 1507 TTTTCTTTTCTCTATCA 1490

RESULT 8
US-10-953-349-10770/c
; Sequence 10770, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10770
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10770

Query Match      77.1%; Score 16.2; DB 6; Length 876;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 860 TTTTCTTTTCTTGTTAAATG 840

RESULT 9
US-10-511-937-506/c
; Sequence 506, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 506
; LENGTH: 1379
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-506

Query Match      77.1%; Score 16.2; DB 6; Length 1379;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 1347 TTTTCTTTTCTCTTTTAAAGG 1327

RESULT 10
US-10-953-349-4335
; Sequence 4335, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4335
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4335

Query Match      77.1%; Score 16.2; DB 6; Length 1429;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
Db 1392 TTTTCTTTTCTCAATTAATG 1412

RESULT 11
US-10-953-349-9239
; Sequence 9239, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9239
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9239

Query Match      77.1%; Score 16.2; DB 6; Length 1508;
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Best Local Similarity 85.7%; Pred. No. 2.7e+02; DB 6; Length 1848;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
DB 1466 TTTTATTCTCAATTAAATG 1486

RESULT 12
US-10-524-648-25/c
; Sequence 25, Application US/10524648
; Publication No. US20060107352A1
; GENERAL INFORMATION:
; APPLICANT: Schopfer, Christel
; APPLICANT: Sauer, Matt
; APPLICANT: Klebsattel, Martin
; APPLICANT: Flachmann, Ralf
; TITLE OF INVENTION: Transgenic expression cassettes for expressing nucleic acids in
; TITLE OF INVENTION: the flower of plants
; FILE REFERENCE: 13173-00002-US
; CURRENT APPLICATION NUMBER: US/10/524,648
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: PCT/EP 03/008394
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: DE 102 38 979.9
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: DE 102 47 599.7
; PRIOR FILING DATE: 2002-02-11
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 1848
; TYPE: DNA
; ORGANISM: Adonis palaeatina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (116)..(1702)
; OTHER INFORMATION: coding for epsilon cyclase
US-10-524-648-25

Query Match 77.1%; Score 16.2; DB 6; Length 1848;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
DB 1838 TTTTCTTTTCTCTATCAATG 1818

RESULT 13
US-10-953-349-8554
; Sequence 8554, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8554
; LENGTH: 1973
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8554

Query Match 77.1%; Score 16.2; DB 6; Length 1973;
Best Local Similarity 85.7%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21

DB 1869 TTTTATTTTCTCTACTAAAG 1889

RESULT 14
US-10-953-349-22034
; Sequence 22034, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22034
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22034

Query Match 77.1%; Score 16.2; DB 6; Length 2082;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATG 21
DB 2008 TTTTCTTTTCTCTTCATG 2028

RESULT 15
US-10-370-959-139/c
; Sequence 139, Application US/10370959
; Publication No. US20060088907A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Williamson, Mark W.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Hunter, John J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: NOVEL 13237, 18480, 2245, 16228, 7677,
; TITLE OF INVENTION: 26320, 46619, 33166, 16836, 46867, 21617, 55562, 39228,
; TITLE OF INVENTION: 62088, 46745, 23155, 21657, 42755, 32229, 22325, 46863 AND
; TITLE OF INVENTION: 32252 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0170MNM
; CURRENT APPLICATION NUMBER: US/10/370,959
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 09/910,150
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,028
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: US 10/251,507
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 09/715,479
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/218,053
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: US 09/644,929
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 60/212,439
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 09/892,870
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,174
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 09/775,117
; PRIOR FILING DATE: 2001-02-01

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 156

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 139

; LENGTH: 2864

; TYPE: DNA

; ORGANISM: Homo Sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (141)... (2675)

US-10-370-959-139

Query Match

Best Local Similarity 77.1%; Score 16.2; DB 6; Length 2864;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATG 21

Db 2860 TTTTCTTTTCTCTATTATG 2840

Search completed: May 31, 2006, 21:22:03

Job time : 9.03704 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 44.6914 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579a-21

Perfect score: 20

Sequence: 1 gttagtgaatactcttggcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	20	100.0	59	3	US-09-109-329-3
C 2	20	100.0	89	3	US-09-109-329-4
C 3	20	100.0	108	3	US-09-109-329-13
C 4	20	100.0	2007	2	US-08-743-6378-169
C 5	20	100.0	2007	3	US-08-526-8408-169
C 6	20	100.0	2028	3	US-09-134-001C-1710
C 7	17.4	87.0	1469	3	US-09-976-594-948
C 8	16.8	84.0	1089	3	US-09-134-000C-2599
C 9	16	80.0	199	3	US-09-533-559-3113
C 10	15.8	79.0	515	3	US-09-621-976-785
C 11	15.8	79.0	601	3	US-09-949-016-13973
C 12	15.8	79.0	601	3	US-09-949-016-183836
C 13	15.8	79.0	601	3	US-09-949-016-183837
C 14	15.8	79.0	601	3	US-09-949-016-186494
C 15	15.8	79.0	601	3	US-09-949-016-202891
C 16	15.8	79.0	913	3	US-09-270-767-9914
C 17	15.8	79.0	9259	3	US-09-949-016-17013
C 18	15.8	79.0	15393	3	US-09-453-7028-191
C 19	15.8	79.0	15393	3	US-10-114-170-191
C 20	15.8	79.0	56678	3	US-09-949-016-17453
C 21	15.8	79.0	60589	3	US-09-949-016-17070
C 22	15.8	79.0	93778	3	US-09-949-016-15096
C 23	15.8	79.0	121234	3	US-09-949-016-14142

24	15.8	79.0	140315	3	US-09-949-016-14141	Sequence 14141, A
C 25	15.8	79.0	147840	3	US-09-949-016-15236	Sequence 15236, A
26	15.4	77.0	601	3	US-09-949-016-89272	Sequence 89272, A
27	15.4	77.0	601	3	US-09-949-016-89273	Sequence 89273, A
C 28	15.4	77.0	792	3	US-09-134-001C-2275	Sequence 2275, Ap
C 29	15.4	77.0	885	3	US-09-134-000C-332	Sequence 332, App
C 30	15.4	77.0	2862	3	US-09-710-279-4341	Sequence 4341, Ap
31	15.4	77.0	4877	3	US-09-566-921-8	Sequence 8, Appli
C 32	15.4	77.0	54649	3	US-09-949-016-15867	Sequence 15867, A
33	15.4	77.0	69701	3	US-09-949-016-14187	Sequence 14187, A
34	15.4	77.0	73308	3	US-09-949-016-16326	Sequence 16326, A
C 35	15.4	77.0	74881	3	US-09-949-016-15545	Sequence 15545, A
C 36	15.4	77.0	74914	3	US-09-949-016-12286	Sequence 12286, A
37	15.4	77.0	8950	3	US-09-949-016-17150	Sequence 17150, A
38	15.4	77.0	94133	3	US-09-949-016-11901	Sequence 11901, A
39	15.4	77.0	94133	3	US-09-949-016-12713	Sequence 12713, A
40	15.4	77.0	94135	3	US-09-949-016-15934	Sequence 15934, A
41	15.4	77.0	94135	3	US-09-949-016-15935	Sequence 15935, A
42	15.4	77.0	94135	3	US-09-949-016-15936	Sequence 15936, A
43	15.4	77.0	94135	3	US-09-949-016-15937	Sequence 15937, A
C 44	15.4	77.0	137753	3	US-09-949-016-17404	Sequence 17404, A
45	15.4	77.0	237510	3	US-09-949-016-14273	Sequence 14273, A

ALIGNMENTS

RESULT 1

US-09-109-329-3/c
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species

US-09-109-329-3

Query Match 100.0%; Score 20; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTGAATATCTTTGCC 20

DB 54 GTTAGTGAATATCTTTGCC 35

RESULT 2

US-09-109-329-4
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-4

Query Match          100.0%; Score 20; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 18 GTTAGTTGAATATCTTTGCC 37

RESULT 3
US-09-109-329-13/c
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-13

Query Match          100.0%; Score 20; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 74 GTTAGTTGAATATCTTTGCC 55

RESULT 4
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
```

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; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match          100.0%; Score 20; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 5
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
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; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 6
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 20; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 1001 GTTAGTTGAATATCTTTGCC 982

RESULT 7
US-09-976-594-948
; Sequence 948, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 948
```

```
; LENGTH: 1469
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 040576.1
US-09-976-594-948

Query Match      87.0%; Score 17.4; DB 3; Length 1469;
Best Local Similarity 94.7%; Pred. No. 47;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 19
Db 363 GTTAGTTGAATATCTTTGCC 381

RESULT 8
US-09-134-000C-2599/c
; Sequence 2599, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2599
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2599

Query Match      84.0%; Score 16.8; DB 3; Length 1089;
Best Local Similarity 90.0%; Pred. No. 90;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
Db 626 GTTAGTTGAATATCTTTGCC 607

RESULT 9
US-09-533-559-3113/c
; Sequence 3113, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3113
; LENGTH: 199
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
```

```

; LOCATION: (1)...(199)
; ; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-3113

Query Match      80.0%; Score 16; DB 3; Length 199;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTTTG 18
DB      94 TTAGTTGAATATCTTTG 78
|||||

RESULT 10
US-09-621-976-785
; Sequence 785, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 785
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 351..515
US-09-621-976-785

Query Match      79.0%; Score 15.8; DB 3; Length 515;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTTAGTTGAATATCTTTGC 19
DB      126 GTCTGTGAATATCTTTGC 144
|||||

RESULT 11
US-09-949-016-123973
; Sequence 123973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123973
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-123973

Query Match      79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTTTGCC 20
DB      326 TAAGTTTAATATCTTTGCC 344
|||||

RESULT 12
US-09-949-016-183836
; Sequence 183836, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183836
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183836

Query Match      79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTTTGCC 20
DB      388 TAAGTTTAATATCTTTGCC 406
|||||

RESULT 13
US-09-949-016-183837
; Sequence 183837, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183837
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183837

Query Match      79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTTTGCC 20
DB      326 TAAGTTTAATATCTTTGCC 344
|||||

```

RESULT 14

US-09-949-016-186494/c
; Sequence 186494, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186494
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-186494

Query Match 79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
DB 243 GTTAGTTCTATATCTTTGC 225

RESULT 15

US-09-949-016-202891/c
; Sequence 202891, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202891
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202891

Query Match 79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
DB 45 GTTAGTTGAATGTTTTC 27

Search completed: May 31, 2006, 21:13:07
Job time : 46.6914 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 519.589 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gttagtgaatactttgcc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	20	3	US-09-865-579A-21
3	20	100.0	39	3	US-09-865-579A-28
4	20	100.0	39	7	US-10-382-328-3
5	20	100.0	1957	9	US-10-479-674-82
6	20	100.0	2007	3	US-09-452-599-169
7	20	100.0	2007	7	US-10-121-120-169
8	20	100.0	2007	9	US-10-479-674-78
9	20	100.0	2007	9	US-10-479-674-90
10	20	100.0	2007	9	US-10-479-674-91
11	20	100.0	2007	9	US-10-121-120-169
12	20	100.0	2028	8	US-10-724-972A-3141
13	17.4	87.0	369	3	US-09-770-791-376
14	17.4	87.0	50807	11	US-10-330-773-781
15	16.8	84.0	350	3	US-09-770-791-701
16	16.8	84.0	403	4	US-09-925-065A-209245
17	16.8	84.0	403	5	US-09-925-065A-209245

C 18	16.8	84.0	419	12	US-10-301-480-296740,
C 19	16.8	84.0	419	12	US-10-301-480-910149
C 20	16.8	84.0	16484	3	US-09-070-927A-158
C 21	16.4	82.0	1095	8	US-10-282-122A-36279
C 22	16.4	82.0	1374	3	US-09-938-842A-4922
C 23	16.4	82.0	1374	3	US-09-938-842A-4922
C 24	16.4	82.0	2001	7	US-10-108-260A-143
C 25	16.4	82.0	2052	13	US-11-097-143-8918
C 26	16.4	82.0	4437	13	US-11-097-143-8917
C 27	16.4	82.0	199	9	US-10-653-047-3113
C 28	16.4	80.0	505	4	US-09-925-065A-831697
C 29	16.4	80.0	505	5	US-09-925-065A-831697
C 30	16.4	80.0	513	4	US-09-925-065A-835390
C 31	16.4	80.0	513	5	US-09-925-065A-835390
C 32	16.4	80.0	560	4	US-09-925-065A-129376
C 33	16.4	80.0	560	5	US-09-925-065A-129376
C 34	16.4	80.0	580	12	US-10-301-480-443275
C 35	16.4	80.0	580	12	US-10-301-480-1056684
C 36	16.4	80.0	582	4	US-09-925-065A-373388
C 37	16.4	80.0	582	5	US-09-925-065A-373388
C 38	16.4	80.0	584	12	US-10-301-480-226005
C 39	16.4	80.0	584	12	US-10-301-480-839414
C 40	16.4	80.0	989	12	US-10-301-480-586303
C 41	16.4	80.0	989	12	US-10-301-480-1199712
C 42	16.4	80.0	998	12	US-10-301-480-583482
C 43	16.4	80.0	998	12	US-10-301-480-1196891
C 44	15.8	79.0	199	8	US-10-424-599-102642
C 45	15.8	79.0	496	4	US-09-925-065A-619276

ALIGNMENTS

RESULT 1

US-09-865-579A-11
; Sequence 11, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-11

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTGCC 20

Db 1 GTTAGTTGAATATCTTTGCC 20

RESULT 2

US-09-865-579A-21
; Sequence 21, Application US/09865579A

; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match 100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 7

US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US2003018073A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 20; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 8

US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 9

US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 10

US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 11
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match 100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 980 GTTAGTTGAATATCTTTGCC 961

RESULT 12
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US2004014734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match 100.0%; Score 20; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
|||||
Db 1001 GTTAGTTGAATATCTTTGCC 982

RESULT 13
US-09-770-791-376/c
; Sequence 376, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; TITLE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(369)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-791-376

Query Match 87.0%; Score 17.4; DB 3; Length 369;
Best Local Similarity 94.7%; Pred. No. 5.6e-02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTGCC 20
|||||
Db 353 TGAGTTGAATATCTTTGCC 335

RESULT 14
US-10-330-773-781
; Sequence 781, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 781
; LENGTH: 50807
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(50807)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-781

Query Match 87.0%; Score 17.4; DB 11; Length 50807;
Best Local Similarity 94.7%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 19
||||| |||||||
DB 50715 GTTAGTTGGATATCTTTGCC 50733

RESULT 15

US-09-770-791-701
; Sequence 701, Application US/09770791
; Patent No. US20020062014A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2029 (PARA-018PRV)
; CURRENT APPLICATION NUMBER: US/09/770,791
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,480
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 701
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-791-701

Query Match 84.0%; Score 16.8; DB 3; Length 350;
Best Local Similarity 90.0%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGCC 20
||| |||||||
DB 281 GTTGGTTGAAGATCTTTGCC 300

Search completed: May 31, 2006, 23:02:25
Job time : 520.589 secs

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 7.65432 Seconds
(without alignments) 307.732 Million cell updates

Title: US-09-865-579A-21

Perfect score: 20

Sequence: 1 gttagtgaatatctttgcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs. 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB geo length: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

**POST-PROCESSING: MINIMUM MATCH 0%
MAXIMUM MATCH 100%**

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:*

- | Database | Table | Field | Value |
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| | | 2: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US06_NEW_PUB.seq.* |
| | | 3: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US07_NEW_PUB.seq.* |
| | | 4: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US08_NEW_PUB.seq.* |
| | | 5: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/PCT_NEW_PUB.seq.* |
| | | 6: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US10_NEW_PUB.seq.* |
| | | 7: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US11_NEW_PUB.seq.* |
| | | 8: | /EMC Celerra_SIDS3/ptodata/2/pubnpa/US6_NEW_PUB.seq.* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	16.4	82.0	1358	6	US-10-953-349-18434	Sequence 18434, A	
c 2	16.4	82.0	2001	7	US-11-293-697-143	Sequence 143, App	
c 3	15.8	79.0	729	7	US-11-217-529-5581	Sequence 5581, Ap	
c 4	15.8	79.0	1542	6	US-10-953-349-27685	Sequence 27685, A	
c 5	15.8	79.0	2676	7	US-11-217-529-5102	Sequence 5102, Ap	
c 6	15.4	77.0	1827	7	US-11-217-529-78826	Sequence 78826, A	
c 7	15.4	77.0	3012	7	US-11-217-529-78176	Sequence 78176, A	
c 8	15	75.0	2778	7	US-11-217-529-5649	Sequence 5649, Ap	
c 9	14.8	74.0	757	6	US-10-488-619-1353	Sequence 1353, Ap	
c 10	14.8	74.0	1617	7	US-11-217-529-1954	Sequence 1954, Ap	
c 11	14.8	74.0	1723	6	US-10-953-349-32641	Sequence 32641, A	
c 12	14.8	74.0	3115	7	US-11-301-554-802	Sequence 802, App	
c 13	14.8	74.0	4637	7	US-11-301-554-804	Sequence 804, App	
c 14	14.8	74.0	4947	7	US-11-217-529-1490	Sequence 1490, Ap	
c 15	14.4	72.0	1257	7	US-11-217-529-1867	Sequence 1867, Ap	
c 16	14.4	72.0	3939	7	US-11-217-529-78219	Sequence 78219, A	
c 17	14.4	72.0	4176	7	US-11-217-529-78349	Sequence 78349, A	
c 18	14.2	71.0	25	7	US-11-217-529-143573	Sequence 143573, A	
c 19	14.2	71.0	381	7	US-11-301-554-755	Sequence 755, App	
c 20	14.2	71.0	381	7	US-11-217-529-173514	Sequence 173514, A	
c 21	14.2	71.0	420	7	US-11-217-529-80348	Sequence 80348, A	
c 22	14.2	71.0	666	6	US-10-953-349-18013	Sequence 18013, A	
c 23	14.2	71.0	963	7	US-11-217-529-76581	Sequence 76581, A	
c 24	14.2	71.0	1148	6	US-10-953-349-4321	Sequence 4321, Ap	
c 25	14.2	71.0	1507	6	US-10-953-349-36240	Sequence 36240, A	

ALIGNMENTS

RESULT 1

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US-10-953-349-18434
; Sequence 18434, Application US/10953349
; Publication NO. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENT
; TITLE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18434
; LENGTH: 1258
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-18434

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Query Match	82.0%	Score 16.4;	DB 6;	Length 1258;
Best Local Similarity	94.4%;	Pred. No. 9.8;		
Matches 17;	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;

Qy 1 GTAGTTGAATATCTTTG 18
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Db 1234 GTAGTTGAATCTCTTTG 1251

RESULT 2

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US-11-293-697-143/C
; Sequence 143, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
;
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-143

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Query Match      82.0%; Score 16.4; DB 7; Length 2001;
Best Local Similarity 94.4%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTGC 19
Db 87 TTATTGGAATATCTTTGC 70

RESULT 3
US-11-217-529-5581/c
; Sequence 5581, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5581
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5581

Query Match      79.0%; Score 15.8; DB 7; Length 729;
Best Local Similarity 89.5%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTTGC 20
Db 627 TTCGTTGAATATCTTTGCC 609

RESULT 4
US-10-953-349-27685/c
; Sequence 27685, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27685
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-27685

Query Match      79.0%; Score 15.8; DB 6; Length 1542;
Best Local Similarity 89.5%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
Db 1050 GTAAGTTGAAATATCTTTGC 1032

RESULT 5
US-11-217-529-5102/c

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; Sequence 5102, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5102
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5102

Query Match      79.0%; Score 15.8; DB 7; Length 2676;
Best Local Similarity 89.5%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTTGC 19
Db 1319 GTTAGTGGATATCTTTGC 1301

RESULT 6
US-11-217-529-78826/c
; Sequence 78826, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78826
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78826

Query Match      77.0%; Score 15.4; DB 7; Length 1827;
Best Local Similarity 94.1%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TAGTTGAATATCTTTGC 19
Db 1361 TAGTTGAAATATCTTTGC 1345

RESULT 7
US-11-217-529-78176/c
; Sequence 78176, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO

```

```
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78176
; LENGTH: 3012
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78176

Query Match          77.0%; Score 15.4; DB 7; Length 3012;
Best Local Similarity 94.1%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTAGTTGAATATCTTT 17
    ||||| ||||| ||||| |||||
Db 101 GTTAGTTGAATATCTTT 85

RESULT 8
US-11-217-529-5649/c
; Sequence 5649, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5649
; LENGTH: 2778
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5649

Query Match          75.0%; Score 15; DB 7; Length 2778;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTAGTTGAATATCTTT 16
    ||||| ||||| ||||| |||||
Db 1159 TTAGTTGAATATCTTT 1145

RESULT 9
US-10-488-619-1353
; Sequence 1353, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1353
; LENGTH: 757
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1353

Query Match          74.0%; Score 14.8; DB 6; Length 757;
Best Local Similarity 88.9%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TAGTTGAATATCTTTGCC 20
    ||||| ||||| ||||| |||||
Db 440 TTGTTGACTATCTTTGCC 457

RESULT 10
US-11-217-529-1954
; Sequence 1954, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1954
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1954

Query Match          74.0%; Score 14.8; DB 7; Length 1617;
Best Local Similarity 88.9%; Pred. No. 59;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TAGTTGAATATCTTTGCC 20
    ||||| ||||| ||||| |||||
Db 133 TATTGAAATCTTTGCC 150

RESULT 11
US-10-953-349-32641/c
; Sequence 32641, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32641
; LENGTH: 1723
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-32641

Query Match          74.0%; Score 14.8; DB 6; Length 1723;
Best Local Similarity 88.9%; Pred. No. 60;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 TTAGTTGAATATCTTTC 19
Db 991 TTAGTTGAATATCTTTC 974

RESULT 12
US-11-301-554-802
; Sequence 802, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 802
; LENGTH: 3115
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-802

Query Match 74.0%; Score 14.8; DB 7; Length 3115;
Best Local Similarity 88.9%; Pred. No. 62;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTC 18
Db 623 GTTAGTTGAATATCTTTC 640

RESULT 13
US-11-301-554-804
; Sequence 804, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong

```

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; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 804
; LENGTH: 4637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-804

Query Match 74.0%; Score 14.8; DB 7; Length 4637;
Best Local Similarity 88.9%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTAGTTGAATATCTTTC 18
Db 2145 GTTAGTTGAATATCTTTC 2162

RESULT 14
US-11-217-529-1490
; Sequence 1490, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: KODAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 1490
; LENGTH: 4947
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1490

Query Match      74.0%; Score 14.8; DB 7; Length 4947;
Best Local Similarity 88.9%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TTAGTTGAATATCTTTC 19
Db      1638 TCAGTTGAATATCTTTC 1655

RESULT 15
US-11-217-529-1867/c
; Sequence 1867, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1867
; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1867

Query Match      72.0%; Score 14.4; DB 7; Length 1257;
Best Local Similarity 93.8%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GTTAGTTGAATATCTT 16
Db      986 GTTATTGAATATCTT 971

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Job time : 8.65432 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 62.5679 Seconds
(without alignments)
837.347 Million cell updates/sec

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Perfect score: 28
Sequence: 1 aaagaaaaagatgcaaaagatttcaa 28

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Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	59	3	US-09-109-329-3
2	28	100.0	89	3	US-09-109-329-4
3	28	100.0	108	3	US-09-109-329-13
4	28	100.0	2007	2	US-08-743-637B-169
5	28	100.0	2007	3	US-08-526-840B-169
6	28	100.0	2028	3	US-09-134-001C-1710
7	21.6	77.1	47	3	US-09-109-329-6
8	20.8	74.3	348	3	US-09-248-796A-1105
9	20.2	72.1	2754	3	US-09-248-796A-5244
10	20	71.4	29	3	US-09-109-957-4
11	20	71.4	29	3	US-09-109-957-5
12	20	71.4	29	3	US-09-109-329-1
13	20	71.4	29	3	US-09-109-329-2
14	20	71.4	29	3	US-09-109-329-5
15	20	71.4	29	3	US-09-109-329-7
16	20	71.4	29	3	US-09-109-329-8
17	20	71.4	36	3	US-09-109-329-14
18	20	71.4	36	3	US-09-109-329-15
19	20	71.4	144	3	US-09-513-999C-17797
20	20	71.4	2003	3	US-10-664-775-3
21	20	71.4	2267	3	US-10-664-775-5
22	20	71.4	2279	3	US-10-664-775-4
23	20	71.4	2316	3	US-09-248-796A-6622

c 24	20	71.4	2715	3	US-10-664-775-1	Sequence 1, Appli
c 25	20	71.4	2775	2	US-08-149-098A-1	Sequence 1, Appli
c 26	20	71.4	2830	3	US-09-221-017B-730	Sequence 730, App
c 27	20	71.4	52174	3	US-09-949-002-573	Sequence 573, App
c 28	20	71.4	52289	3	US-09-949-002-720	Sequence 720, App
c 29	20	71.4	83516	3	US-09-949-016-15378	Sequence 15378, A
c 30	20	71.4	98567	3	US-09-949-016-11750	Sequence 11750, A
c 31	20	71.4	100567	3	US-09-949-016-16934	Sequence 16934, A
c 32	20	71.4	117937	3	US-09-949-016-12762	Sequence 12762, A
c 33	20	71.4	117937	3	US-09-949-016-15775	Sequence 15775, A
c 34	20	71.4	183770	3	US-09-949-016-15494	Sequence 15494, A
c 35	20	71.4	317366	3	US-09-949-016-16001	Sequence 16001, A
c 36	19.8	70.7	249	3	US-09-248-796A-9823	Sequence 9823, Ap
c 37	19.8	70.7	249	3	US-09-248-796A-12455	Sequence 12455, A
c 38	19.8	70.7	249	3	US-09-248-796A-12815	Sequence 12815, A
c 39	19.8	70.7	249	3	US-09-248-796A-13043	Sequence 13043, A
c 40	19.8	70.7	1747	2	US-07-808-455A-2	Sequence 2, Appli
c 41	19.6	70.0	143	5	US-09-974-300-3560	Sequence 3560, Ap
c 42	19.6	70.0	601	3	US-09-949-016-31698	Sequence 31698, A
c 43	19.6	70.0	601	3	US-09-949-016-87733	Sequence 87733, A
c 44	19.6	70.0	601	3	US-09-949-016-150341	Sequence 150341,
c 45	19.6	70.0	601	3	US-09-949-016-199396	Sequence 199396,

ALIGNMENTS

RESULT 1
US-09-109-329-3
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-3

Query Match 100.0%; Score 28; DB 3; Length 59;
Best Local Similarity 85.7%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 4;

QY 1 AAAGAAAAAGATGCCAAAGATATTCAA 28
|||||:|||||:|||||:|||||:|||||:
Db 22 AAAGAAAAAGATGCCAAAGAUUCAA 49

RESULT 2
US-09-109-329-4/c
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-4

Query Match          100.0%; Score 28; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 50 AAAGAAAAAGATGCGCAAGATATTCAA 23

RESULT 3
US-09-109-329-13
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE OF INVENTION: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-13

Query Match          100.0%; Score 28; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 42 AAAGAAAAAGATGCGCAAGATATTCAA 69

RESULT 4
US-08-743-637B-169
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
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; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5500
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match          100.0%; Score 28; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 5
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
```

REFERENCE/DOCKET NUMBER: 850586.90012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 948 AAAGAAAAAGATGGCAAGATATTCAA 975

RESULT 6

US-09-134-001C-1710
Sequence 1710, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 1710
LENGTH: 2028
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
FEATURE:
NAME/KEY: unsure
LOCATION: (52)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 969 AAAGAAAAAGATGGCAAGATATTCAA 996

RESULT 7

US-09-109-329-6
Sequence 6, Application US/09109329
Patent No. 6503709
GENERAL INFORMATION:
APPLICANT: Bekkaoui, Faouzi
APPLICANT: Cloney, Lynn P.
TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
TITLE OF INVENTION: STAPHYLOCOCCI
FILE REFERENCE: 480094.424
CURRENT APPLICATION NUMBER: US/09/109,329
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 47

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-6

Query Match 77.1%; Score 21.6; DB 3; Length 47;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGGCAAGATATTCAA 28
Db 10 AAAGAAAAAGATGGCAAGAAAAAAA 37

RESULT 8

US-09-248-796A-1105
Sequence 1105, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 1105
LENGTH: 348
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-1105

Query Match 74.3%; Score 20.8; DB 3; Length 348;
Best Local Similarity 91.7%; Pred. No. 80;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAAAAGATGGCAAGATATTCAA 28
Db 142 AAAGAAGATGGCAAGATATTGAA 165

RESULT 9

US-09-248-796A-5244
Sequence 5244, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5244
LENGTH: 2754
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-5244

Query Match 72.1%; Score 20.2; DB 3; Length 2754;
Best Local Similarity 88.0%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-5

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAAAAAGATGGCAAG 20
DB 10 AAAGAAAAAGATGGCAAG 29

RESULT 15
US-09-109-329-7
; Sequence 7, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-7

Query Match 71.4%; Score 20; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAGAAAAAGATGGCAAG 20
DB 10 AAAGAAAAAGATGGCAAG 29

Search completed: May 31, 2006, 21:13:04
Job time : 63.5679 secs

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: May 31, 2006, 21:16:53 ; Search time 727.424 Seconds
 (without alignments)
 472.976 Million cell updates/sec

Title: US-09-865-579A-22
 Perfect score: 28
 Sequence: 1 aaagaaaaagatgcaagatattcaa 28

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA Main:
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 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query		Length	DB	ID	Description		
		Match	%						
1	28	100.0		28	3	US-09-865-579A-22	Sequence 22, Appl		
C 2	28	100.0		39	3	US-09-865-579A-28	Sequence 28, Appl		
C 3	28	100.0		39	7	US-10-382-328-3	Sequence 3, Appl		
4	28	100.0		1957	9	US-10-479-674-82	Sequence 82, Appl		
5	28	100.0		2007	3	US-09-452-599-169	Sequence 169, Appl		
6	28	100.0		2007	7	US-10-121-120-169	Sequence 169, Appl		
7	28	100.0		2007	9	US-10-479-674-78	Sequence 78, Appl		
8	28	100.0		2007	9	US-10-479-674-90	Sequence 90, Appl		
9	28	100.0		2007	9	US-10-479-674-91	Sequence 91, Appl		
10	28	100.0		2007	9	US-10-121-120-169	Sequence 169, Appl		
11	28	100.0		2028	8	US-10-724-972A-3141	Sequence 3141, Appl		
C 12	22.8	81.4		618	9	US-10-468-488-389	Sequence 389, Appl		
C 13	21.6	77.1		576	12	US-10-301-480-16890	Sequence 16890, Appl		
C 14	21.6	77.1		576	12	US-10-301-480-16891	Sequence 16891, Appl		
C 15	21.6	77.1		576	12	US-10-301-480-310371	Sequence 310371, Appl		
C 16	21.6	77.1		576	12	US-10-301-480-310372	Sequence 310372, Appl		
C 17	21.6	77.1		576	12	US-10-301-480-630299	Sequence 630299, Appl		

C 18	21.6	77.1	576	12	US-10-301-480-630300	Sequence 630300, A					
C 19	21.6	77.1	576	12	US-10-301-480-923780	Sequence 923780, A					
C 20	21.6	77.1	576	12	US-10-301-480-923781	Sequence 923781, A					
21	21.6	77.1	586	4	US-09-925-065A-225842	Sequence 225842, A					
22	21.6	77.1	586	4	US-09-925-065A-225843	Sequence 225843, A					
23	21.6	77.1	586	5	US-09-925-065A-225842	Sequence 225842, A					
24	21.6	77.1	586	5	US-09-925-065A-225843	Sequence 225843, A					
C 25	21.6	77.1	641	6	US-10-027-632-83702	Sequence 83702, A					
C 26	21.6	77.1	641	6	US-10-027-632-83703	Sequence 83703, A					
C 27	21.6	77.1	641	6	US-10-027-632-83704	Sequence 83704, A					
C 28	21.6	77.1	641	6	US-10-027-632-302613	Sequence 302613, A					
C 29	21.6	77.1	641	6	US-10-027-632-302614	Sequence 302614, A					
C 30	21.6	77.1	641	6	US-10-027-632-302615	Sequence 302615, A					
C 31	21.6	77.1	641	7	US-10-027-632-83702	Sequence 83702, A					
C 32	21.6	77.1	641	7	US-10-027-632-83703	Sequence 83703, A					
C 33	21.6	77.1	641	7	US-10-027-632-83704	Sequence 83704, A					
C 34	21.6	77.1	641	7	US-10-027-632-302613	Sequence 302613, A					
C 35	21.6	77.1	641	7	US-10-027-632-302614	Sequence 302614, A					
C 36	21.6	77.1	641	7	US-10-027-632-302615	Sequence 302615, A					
C 37	21.6	77.1	665	6	US-10-027-632-34239	Sequence 34239, A					
C 38	21.6	77.1	665	6	US-10-027-632-34240	Sequence 34240, A					
C 39	21.6	77.1	665	7	US-10-027-632-34239	Sequence 34239, A					
C 40	21.6	77.1	665	7	US-10-027-632-34240	Sequence 34240, A					
C 41	21.6	77.1	665	7	US-10-027-632-34239	Sequence 34239, A					
C 42	21.6	77.1	665	7	US-10-027-632-34241	Sequence 34241, A					
C 43	21.6	77.1	1277	4	US-09-925-065A-686913	Sequence 686913, A					
C 44	21.6	77.1	1277	4	US-09-925-065A-716679	Sequence 716679, A					
C 45	21.6	77.1	1277	5	US-09-925-065A-686913	Sequence 686913, A					

ALIGNMENTS

RESULT 1

US-09-865-579A-22
 ; Sequence 22, Application US/09865579A
 ; Patent No. US20020098492A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Taya, Toshiki
 ; APPLICANT: Ishiguro, Takahiko
 ; APPLICANT: Saito, Juichi
 ; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
 ; FILE REFERENCE: 9558-003-27
 ; CURRENT APPLICATION NUMBER: US/09/865,579A
 ; PRIOR FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: JP 2000-163149
 ; PRIOR FILING DATE: 2000-05-29
 ; PRIOR APPLICATION NUMBER: JP 2000-179394
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 22
 ; LENGTH: 28
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-09-865-579A-22
 Query Match 100.0%; Score 28; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AAAGAAAAGATGCAAGATATTCAA 28
 Db 1 AAAGAAAAGATGCAAGATATTCAA 28
 RESULT 2
 US-09-865-579A-28/c
 ; Sequence 28, Application US/09865579A
 ; Patent No. US20020098492A1

```
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-28

Query Match      100.0%; Score 28; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGCGCAAGATATTCAA 28
Db 33 AAAGAAAAAAGATGCGCAAGATATTCAA 6

RESULT 3
US-10-382-328-3/c
; Sequence 3, Application US/10392328
; Publication No. US20030219729A1
; GENERAL INFORMATION:
; APPLICANT: YASUKAWA, Kiyohi
; TITLE OF INVENTION: UNARY MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS USE
; FILE REFERENCE: Q74425
; CURRENT APPLICATION NUMBER: US/10/382,328
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: JP 2002-071841
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-382-328-3

Query Match      100.0%; Score 28; DB 7; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGCGCAAGATATTCAA 28
Db 33 AAAGAAAAAAGATGCGCAAGATATTCAA 6

RESULT 4
US-10-479-674-82
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
```

```
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 28; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGCGCAAGATATTCAA 28
Db 898 AAAGAAAAAAGATGCGCAAGATATTCAA 925

RESULT 5
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAAGATGCGCAAGATATTCAA 28
Db 948 AAAGAAAAAAGATGCGCAAGATATTCAA 975

RESULT 6
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
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; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 7
US-10-479-674-78
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 8
US-10-479-674-90
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90
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Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975
```

```
RESULT 9
US-10-479-674-91
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91
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Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
   |||||
Db 948 AAAGAAAAAGATGCGCAAGATATTCAA 975
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RESULT 10
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169
```

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Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
 |||||
 DB 948 AAAGAAAAAGATGCGCAAGATATTCAA 975

RESULT 11
 US-10-724-972A-3141
 ; Sequence 3141, Application US/10724972A
 ; Publication No. US20040147734A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Doucette-Stamm, Lynn
 ; APPLICANT: Bush, David
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; CURRENT APPLICATION NUMBER: US/10/724, 972A
 ; CURRENT FILING DATE: 2003-12-01
 ; PRIOR APPLICATION NUMBER: 09/450, 969
 ; PRIOR FILING DATE: 1999-11-29
 ; PRIOR APPLICATION NUMBER: 09/134, 001
 ; PRIOR FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: 60/064, 964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: 60/055, 779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 7544
 ; SEQ ID NO 3141
 ; LENGTH: 2028
 ; TYPE: DNA
 ; ORGANISM: S.epidermidis
 US-10-724-972A-3141

Query Match 100.0%; Score 28; DB 8; Length 2028;
 Best Local Similarity 100.0%; Pred. No. 5.9; Mismatches 0; Indels 0; Gaps 0;
 Matches 28; Conservative 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
 |||||
 DB 969 AAAGAAAAAGATGCGCAAGATATTCAA 996

RESULT 12
 US-10-468-488-389/c
 ; Sequence 389, Application US/10468488
 ; Publication No. US20040234968A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CROTEAU, Rodney B.
 ; APPLICANT: LANGE, Bernd M.
 ; APPLICANT: WILDUNG, Mark R.
 ; TITLE OF INVENTION: PLANT OIL GLAND NUCLEIC ACID MOLECULES, AND METHODS OF
 ; FILE REFERENCE: WSUR121565
 ; CURRENT APPLICATION NUMBER: US/10/468, 488
 ; CURRENT FILING DATE: 2003-08-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/02567
 ; PRIOR FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 60/177, 264
 ; PRIOR FILING DATE: 2000-01-20
 ; NUMBER OF SEQ ID NOS: 473
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 389
 ; LENGTH: 618
 ; TYPE: DNA
 ; ORGANISM: Mentha piperita
 US-10-468-488-389

Query Match 81.4%; Score 22.8; DB 9; Length 618;
 Best Local Similarity 92.3%; Pred. No. 3.3e+02;
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCC 26
 |||||
 DB 552 AAAGAAAAAGATGCGCAAGATATTCC 527

RESULT 13
 US-10-301-480-16890/c
 ; Sequence 16890, Application US/10301480
 ; Publication No. US20060057564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
 ; FILE REFERENCE: 108827.137
 ; CURRENT APPLICATION NUMBER: US/10/301, 480
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 10/215, 598
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US 60/311, 695
 ; PRIOR FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 1226818
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16890
 ; LENGTH: 576
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-301-480-16890

Query Match 77.1%; Score 21.6; DB 12; Length 576;
 Best Local Similarity 85.7%; Pred. No. 8.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
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 DB 130 AAAGAAAAAGATGCGCAAGATATTCAA 103

RESULT 14
 US-10-301-480-16891/c
 ; Sequence 16891, Application US/10301480
 ; Publication No. US20060057564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
 ; FILE REFERENCE: 108827.137
 ; CURRENT APPLICATION NUMBER: US/10/301, 480
 ; CURRENT FILING DATE: 2002-11-21
 ; PRIOR APPLICATION NUMBER: US 10/215, 598
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US 60/311, 695
 ; PRIOR FILING DATE: 2001-08-10
 ; NUMBER OF SEQ ID NOS: 1226818
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16891
 ; LENGTH: 576
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-301-480-16891

Query Match 77.1%; Score 21.6; DB 12; Length 576;
 Best Local Similarity 85.7%; Pred. No. 8.6e+02;
 Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
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 DB 130 AAAGAAAAAGATGCGCAAGATATTCAA 103

RESULT 15
 US-10-301-480-310371/c
 ; Sequence 310371, Application US/10301480
 ; Publication No. US20060057564A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 10.716 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-22
Perfect score: 28
Sequence: 1 aaagaaaaagatgcaaaagatttcaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19	67.9	644	6	US-10-953-349-29445
3	19	67.9	987	7	US-11-217-529-191045
4	19	67.9	1289	6	US-10-953-349-23125
5	19	67.9	1448	6	US-10-953-349-17539
6	19	67.9	1578	7	US-11-217-529-78085
7	18.6	66.4	549	7	US-11-217-529-79689
8	18.6	66.4	1116	7	US-11-217-529-2228
9	18.6	66.4	2568	7	US-11-217-529-77262
10	18.4	65.7	1574	6	US-10-488-619-2193
11	18.4	65.7	1664	6	US-10-953-349-8516
12	18.4	65.7	1777	6	US-10-953-349-8747
13	18.4	65.7	1801	6	US-10-953-349-9366
14	18.4	65.7	2490	7	US-11-293-697-401
15	18.4	65.7	3949	7	US-11-293-697-1211
16	18.4	65.7	4422	7	US-11-217-529-3003
17	18.4	65.7	4422	7	US-11-217-529-3003
18	18.2	65.0	682	6	US-10-488-619-2641
19	18.2	65.0	2667	7	US-11-217-529-81093
20	18	64.3	1176	7	US-11-217-529-80878
21	18	64.3	1187	6	US-10-953-349-1243
22	17.8	63.6	387	7	US-11-217-529-5325
23	17.8	63.6	1281	7	US-11-217-529-3303
24	17.8	63.6	2140	7	US-11-293-697-1100
25	17.6	62.9	558	6	US-10-953-349-28180

26	17.6	62.9	1407	7	US-11-217-529-535	Sequence 535, App
27	17.6	62.9	1476	6	US-10-953-349-33236	Sequence 33236, A
28	17.6	62.9	2019	7	US-11-217-529-79218	Sequence 79218, A
29	17.6	62.9	2021	6	US-10-953-349-14571	Sequence 14571, A
30	17.4	62.1	600	7	US-11-217-529-466	Sequence 466, App
31	17.4	62.1	750	7	US-11-217-529-81373	Sequence 81373, A
32	17.4	62.1	791	6	US-10-953-349-21923	Sequence 21923, A
33	17.4	62.1	1127	6	US-10-953-349-1769	Sequence 1769, App
34	17.4	62.1	1250	6	US-10-473-173-69	Sequence 69, Appl
35	17.4	62.1	1661	6	US-10-953-349-1884	Sequence 1884, App
36	17.4	62.1	1700	6	US-10-953-349-2065	Sequence 2065, App
37	17.4	62.1	1716	7	US-11-217-529-77529	Sequence 77529, A
38	17.4	62.1	1854	7	US-11-217-529-78308	Sequence 78308, A
39	17.4	62.1	2697	7	US-11-217-529-883	Sequence 883, App
40	17.4	62.1	2853	6	US-10-953-349-6444	Sequence 6444, App
41	17.4	62.1	4098	6	US-10-510-508-2	Sequence 2, Appl1
42	17.4	62.1	4260	7	US-11-217-529-2191	Sequence 2191, App
43	17.4	62.1	6891	7	US-11-251-724-2	Sequence 2, Appl1
44	17.2	61.4	25	7	US-11-217-529-11035	Sequence 11035, A
45	17.2	61.4	25	7	US-11-217-529-163683	Sequence 163683, A

ALIGNMENTS

RESULT 1
US-11-217-529-75813
; Sequence 75813, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75813
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75813
Query Match 67.9%; Score 19; DB 7; Length 522;
Best Local Similarity 81.5%; Pred. No. 35;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 AAGAAAAAGATGCGCAAGATATTCAA 28
DB 442 AAGAAAAAGATGCGCAAAAAATAAGAA 468
RESULT 2
US-10-953-349-29445/c
; Sequence 29445, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29445

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; LENGTH: 644
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-953-349-29445

Query Match          67.9%; Score 19; DB 6; Length 644;
Best Local Similarity 81.5%; Pred. No. 36;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGAAAAAAGATGGCAAGAATATTCAA 28
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Db      428 AAGATGAACATGGCAAGAATTTCCA 402

RESULT 3
US-11-217-529-191045
; Sequence 191045, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191045
; LENGTH: 987
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-191045

Query Match          67.9%; Score 19; DB 7; Length 987;
Best Local Similarity 81.5%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 AAGAAAAAAGATGGCAAGAATATTC 27
      ||||| ||||| ||||| |||||
Db      456 AATGA AAAAGATGACAAGGTTATTGA 482

RESULT 4
US-10-953-349-23125
; Sequence 23125, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23125
; LENGTH: 1289
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-23125

Query Match          67.9%; Score 19; DB 6; Length 1289;
Best Local Similarity 81.5%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGAAAAAAGATGGCAAGAATATTCAA 28
      ||||| ||||| ||||| |||||

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; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 79689
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79689

Query Match      66.4%; Score 18.6; DB 7; Length 549;
Best Local Similarity 84.0%; Pred. No. 50;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATT 25
Db 412 AAAGAACAACTAAGCGCAAGATATT 436

RESULT 8
US-11-217-529-2228
; Sequence 2228, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2228
; LENGTH: 1116
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2228

Query Match      66.4%; Score 18.6; DB 7; Length 1116;
Best Local Similarity 84.0%; Pred. No. 56;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATT 25
Db 147 AAAGAAATACGAAGGCGCAAGATATT 171

RESULT 9
US-11-217-529-77262
; Sequence 77262, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 77262
; LENGTH: 2568
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77262

Query Match      66.4%; Score 18.6; DB 7; Length 2568;
Best Local Similarity 84.0%; Pred. No. 64;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAGAAAAAGATGCGCAAGATATT 26
Db 1261 ATGAAAAACGATGGTAAAAATATT 1285

RESULT 10
US-10-488-619-2193
; Sequence 2193, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations and Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2193
; LENGTH: 545
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2193

Query Match      65.7%; Score 18.4; DB 6; Length 545;
Best Local Similarity 78.6%; Pred. No. 59;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
Db 123 AAAGAAAAAGATGCGAAGCATAAAAA 150

RESULT 11
US-10-953-349-8516/c
; Sequence 8516, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 8516
; LENGTH: 1574
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8516

Query Match      65.7%; Score 18.4; DB 6; Length 1574;
Best Local Similarity 78.6%; Pred. No. 70;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AAAGAAAAAGATGCGCAAGATATTCAA 28
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Db      1499 AGAAACAAAGATGAAAGAGATTCAA 1472
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RESULT 12
US-10-953-349-8747/c
; Sequence 8747, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8747
; LENGTH: 1664
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-8747

Query Match      65.7%; Score 18.4; DB 6; Length 1664;
Best Local Similarity 78.6%; Pred. No. 71;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
Db      1571 AAAGAAACAGATATATAACATATGCAA 1544

RESULT 13
US-10-953-349-9966/c
; Sequence 9966, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9966
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9966

Query Match      65.7%; Score 18.4; DB 6; Length 1777;
Best Local Similarity 78.6%; Pred. No. 72;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
Db      403 AGAGAAAGAGACGACCAAGATAGTCAA 376

RESULT 14
US-10-953-349-935/c
; Sequence 935, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 935
; LENGTH: 1801
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-935

Query Match      65.7%; Score 18.4; DB 6; Length 1801;
Best Local Similarity 78.6%; Pred. No. 72;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
|||||
Db      430 AGAGAAAGAGACGACCAAGATAGTCAA 403

RESULT 15
US-11-293-697-401
; Sequence 401, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 401
; LENGTH: 2490
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-401

Query Match      65.7%; Score 18.4; DB 7; Length 2490;
Best Local Similarity 78.6%; Pred. No. 76;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 AAAGAAAAAGATGCGCAAGATATTCAA 28
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Db      695 AAACAATTAATTGTCAAGAAATTCAA 722

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Job time : 10.716 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-09-865-579A-23

Perfect score: 20

Sequence: 1 ttctttttatcttcggta 20

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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C 2	20	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	20	100.0	2028	3	US-09-134-001C-1710 Sequence 1710, Ap
C 4	17.4	87.0	601	3	US-09-949-016-82367 Sequence 82367, A
C 5	17.4	87.0	601	3	US-09-949-016-82368 Sequence 82368, A
C 6	17.4	87.0	601	3	US-09-949-016-82369 Sequence 82369, A
C 7	17.4	87.0	601	3	US-09-949-016-82370 Sequence 82370, A
C 8	17.4	87.0	601	3	US-09-949-016-187537 Sequence 187537, A
C 9	17.4	87.0	601	3	US-09-949-016-187538 Sequence 187538, A
C 10	17.4	87.0	601	3	US-09-949-016-187539 Sequence 187539, A
C 11	17.4	87.0	601	3	US-09-949-016-187540 Sequence 187540, A
C 12	17.4	87.0	910	5	US-09-974-300-1089 Sequence 1089, Ap
C 13	17.4	87.0	98962	3	US-09-949-016-14133 Sequence 14133, A
C 14	17.4	87.0	102884	3	US-09-949-016-17100 Sequence 17100, A
C 15	16.8	84.0	601	3	US-09-949-016-153600 Sequence 153600, A
C 16	16.8	84.0	795	3	US-09-248-796A-3644 Sequence 3644, Ap
C 17	16.8	84.0	823	3	US-09-949-016-2333 Sequence 2333, Ap
C 18	16.8	84.0	1214	3	US-09-506-286B-15 Sequence 15, Appl
C 19	16.8	84.0	1214	3	US-09-506-286B-18 Sequence 18, Appl
C 20	16.8	84.0	1214	3	US-09-762-861B-15 Sequence 15, Appl
C 21	16.8	84.0	1214	3	US-09-762-861B-18 Sequence 18, Appl
C 22	16.8	84.0	1214	3	US-10-065-133A-15 Sequence 15, Appl
C 23	16.8	84.0	1214	3	US-10-065-133A-18 Sequence 18, Appl

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C 24 16.8 84.0 1214 3 US-10-434-811A-15 Sequence 15, Appl
C 25 16.8 84.0 1214 3 US-10-434-811A-18 Sequence 18, Appl
C 26 16.8 84.0 1241 3 US-09-506-286B-13 Sequence 13, Appl
C 27 16.8 84.0 1241 3 US-09-506-286B-16 Sequence 16, Appl
C 28 16.8 84.0 1241 3 US-09-762-861B-13 Sequence 13, Appl
C 29 16.8 84.0 1241 3 US-09-762-861B-16 Sequence 16, Appl
C 30 16.8 84.0 1241 3 US-10-065-133A-13 Sequence 13, Appl
C 31 16.8 84.0 1241 3 US-10-065-133A-16 Sequence 16, Appl
C 32 16.8 84.0 1241 3 US-10-434-811A-13 Sequence 13, Appl
C 33 16.8 84.0 1241 3 US-10-434-811A-16 Sequence 16, Appl
C 34 16.8 84.0 2277 3 US-09-506-286B-46 Sequence 46, Appl
C 35 16.8 84.0 2277 3 US-09-506-286B-49 Sequence 49, Appl
C 36 16.8 84.0 2277 3 US-10-065-133A-46 Sequence 46, Appl
C 37 16.8 84.0 2277 3 US-10-065-133A-49 Sequence 49, Appl
C 38 16.8 84.0 2341 3 US-09-506-286B-44 Sequence 44, Appl
C 39 16.8 84.0 2341 3 US-09-506-286B-47 Sequence 47, Appl
C 40 16.8 84.0 2341 3 US-10-065-133A-44 Sequence 44, Appl
C 41 16.8 84.0 2341 3 US-10-065-133A-47 Sequence 47, Appl
C 42 16.8 84.0 3116 3 US-09-710-279-3721 Sequence 3721, Ap
C 43 16.8 84.0 3598 3 US-09-710-279-4216 Sequence 4216, Ap
C 44 16.8 84.0 12951 3 US-09-949-016-14075 Sequence 14075, A
C 45 16.8 84.0 15071 3 US-09-710-279-2963 Sequence 2963, Ap

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ALIGNMENTS

RESULT 1

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US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

```

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match      100.0%; Score 20; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
    |||||||
Db 1167 TTCTTTTATCTTCGGTTA 1148

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSER: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
    |||||||
Db 1167 TTCTTTTATCTTCGGTTA 1148

RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
```

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 20; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
    |||||||
Db 1188 TTCTTTTATCTTCGGTTA 1169

RESULT 4
US-09-949-016-82367
; Sequence 82367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82367
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-82367

Query Match      87.0%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
    |||||||
Db 129 TTCTTTTATCTTCGGTT 147

RESULT 5
US-09-949-016-82368
; Sequence 82368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82368
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82368

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Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%	Pred. NO. 4e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			

Qy 1 T T C T T T T T T A T C T T C G G T T 19
db 130 T T C T T T T T T A T C T T C T G T T 148

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RESULT 6
US-09-949-016-82369
; Sequence 82369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWLEDGE
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 82369
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82369

```

Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%	Pred. No. 4e+02;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 1 T T C T T T T T T A T C T T C G G T T 19
|||
Db 255 T T C T T T T T T A T C T T C T G T T 273

RESULT 7
US-09-949-016-82370
; Sequence 82370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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, PRIOR APPLICATION NUMBER: 60/237,768
, PRIOR FILING DATE: 2000-10-03
, PRIOR APPLICATION NUMBER: 60/231,498
, PRIOR FILING DATE: 2000-09-08
, NUMBER OF SEQ ID NOS: 207012
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 82370
, LENGTH: 601
, TYPE: DNA
, ORGANISM: Human
US-09-949-016-82370

```

Query Match 87.0%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels

Qy 1 TTCTTTTATCTTCGGT 19
Db 479 TTCTTTTATCTTCGT 497

```

RESULT 8
US-09-949-016-187537
; Sequence 187537, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187537
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187537

```

Query Match	87.0%	Score 17.4;	DB 3;	Length 601;
Best Local Similarity	94.7%;	Pred. No. 4e+02;		
Matches 18;	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;

QY 1 TTCCTTTTATCTTCGGTT 19
|||
Db 129 TTCCTTTTATCTTCGTT 147

RESULT 9
US-09-349-016-187538
; Sequence 187538, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187538
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187538

Query Match      87.0%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TTCTTTTATCTTCGGTT 19
|||
130 TTCTTTTATCTTCGTT 148

RESULT 10
US-09-949-016-187539
; Sequence 187539, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187539
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187539

Query Match      87.0%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TTCTTTTATCTTCGGTT 19
|||
255 TTCTTTTATCTTCGTT 273

RESULT 11
US-09-949-016-187540
; Sequence 187540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187540
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-187540

Query Match      87.0%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TTCTTTTATCTTCGGTT 19
|||
552 TCCTTTTATCTTCGTT 534

RESULT 12
US-09-974-300-1089/c
; Sequence 1089, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1089
; LENGTH: 910
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-1089

Query Match      87.0%; Score 17.4; DB 5; Length 910;
Best Local Similarity 94.7%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TTCTTTTATCTTCGGTT 19
|||
552 TCCTTTTATCTTCGTT 534

RESULT 13
US-09-949-016-14133/c
; Sequence 14133, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14133
; LENGTH: 98962
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(98962)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14133

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Query Match 87.0%; Score 17.4; DB 3; Length 98962;
 Best Local Similarity 94.7%; Pred. No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGTT 19
 |||||
 Db 47622 TTCTTTTATCTTCGTT 47604

RESULT 14
 US-09-949-016-17100/c
 ; Sequence 17100, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 17100
 ; LENGTH: 102884
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)...(102884)
 ; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17100

Query Match 87.0%; Score 17.4; DB 3; Length 102884;
 Best Local Similarity 94.7%; Pred. No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGTT 19
 |||||
 Db 47622 TTCTTTTATCTTCGTT 47604

RESULT 15
 US-09-949-016-153600
 ; Sequence 153600, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 153600
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human

US-09-949-016-153600

Query Match 84.0%; Score 16.8; DB 3; Length 601;

Best Local Similarity 90.0%; Pred. No. 6.9e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGTTA 20
 |||||
 Db 320 TTCTTTTATCTTCGTTA 339

Search completed: May 31, 2006, 21:12:56
 Job time : 45.6914 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 519.589 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-23
Perfect score: 20
Sequence: 1 tctcttttatcttcggtta 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	20	100.0	20	3	US-09-865-579A-13	Sequence 13, Appl
2	20	100.0	20	3	US-09-865-579A-23	Sequence 23, Appl
3	20	100.0	20	7	US-10-382-328-2	Sequence 2, Appl
4	20	100.0	85	10	US-10-995-051-19	Sequence 19, Appl
5	20	100.0	86	10	US-10-995-051-30	Sequence 30, Appl
C 6	20	100.0	281	10	US-10-995-051-14	Sequence 14, Appl
C 7	20	100.0	560	10	US-10-478-633A-151	Sequence 151, Appl
C 8	20	100.0	652	9	US-10-479-674-30	Sequence 30, Appl
C 9	20	100.0	657	9	US-10-479-674-27	Sequence 27, Appl
C 10	20	100.0	744	9	US-10-479-674-29	Sequence 29, Appl
C 11	20	100.0	782	9	US-10-479-674-28	Sequence 28, Appl
C 12	20	100.0	1858	9	US-10-479-674-181	Sequence 181, Appl
C 13	20	100.0	1861	9	US-10-479-674-192	Sequence 192, Appl
C 14	20	100.0	1861	9	US-10-479-674-193	Sequence 193, Appl
C 15	20	100.0	1957	9	US-10-479-674-82	Sequence 82, Appl
C 16	20	100.0	2007	3	US-09-452-599-169	Sequence 169, Appl
C 17	20	100.0	2007	7	US-10-121-120-169	Sequence 169, Appl

C 18	20	100.0	2007	9	US-10-479-674-78	Sequence 78, Appl
C 19	20	100.0	2007	9	US-10-479-674-90	Sequence 90, Appl
C 20	20	100.0	2007	9	US-10-479-674-91	Sequence 91, Appl
C 21	20	100.0	2007	9	US-10-121-120-169	Sequence 169, Appl
C 22	20	100.0	2028	8	US-10-724-972A-3141	Sequence 3141, App
C 23	20	100.0	2386	9	US-10-479-674-224	Sequence 224, App
C 24	20	100.0	2410	9	US-10-479-674-190	Sequence 190, App
C 25	20	100.0	2436	9	US-10-479-674-31	Sequence 31, Appl
C 26	20	100.0	3101	9	US-10-479-674-195	Sequence 195, App
C 27	20	100.0	3506	9	US-10-479-674-196	Sequence 196, App
C 28	18.4	92.0	86	10	US-10-995-051-13	Sequence 13, Appl
C 29	17.4	87.0	277	10	US-10-499-352A-301	Sequence 301, App
C 30	17.4	87.0	439	6	US-10-027-632-73528	Sequence 73528, A
C 31	17.4	87.0	439	6	US-10-027-632-75071	Sequence 75071, A
C 32	17.4	87.0	439	6	US-10-027-632-108842	Sequence 108842, A
C 33	17.4	87.0	439	7	US-10-027-632-73528	Sequence 73528, A
C 34	17.4	87.0	439	7	US-10-027-632-75071	Sequence 75071, A
C 35	17.4	87.0	439	7	US-10-027-632-108842	Sequence 108842, A
C 36	17.4	87.0	546	4	US-09-925-065A-475594	Sequence 475594, A
C 37	17.4	87.0	546	5	US-09-925-065A-475594	Sequence 475594, A
C 38	17.4	87.0	570	10	US-10-501-282-613	Sequence 613, App
C 39	17.4	87.0	582	10	US-10-499-352A-303	Sequence 303, App
C 40	17.4	87.0	614	12	US-10-301-480-197304	Sequence 197304, A
C 41	17.4	87.0	614	12	US-10-301-480-810713	Sequence 810713, A
C 42	17.4	87.0	633	10	US-10-499-352A-302	Sequence 302, App
C 43	17.4	87.0	639	4	US-09-925-065A-96207	Sequence 96207, A
C 44	17.4	87.0	639	5	US-09-925-065A-96207	Sequence 96207, A
C 45	17.4	87.0	910	3	US-09-974-300-1089	Sequence 1089, App

ALIGNMENTS

RESULT 1

US-09-865-579A-13
; Sequence 13, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiko
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saico, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene
US-09-865-579A-13

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGTTA 20

DB 1 TTCTTTTATCTTCGTTA 20

RESULT 2

US-09-865-579A-23
; Sequence 23, Application US/09865579A

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; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-23

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Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTCTTTTATCTTCGGTTA 20
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Db 1 TTCTTTTATCTTCGGTTA 20

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RESULT 3
US-10-382-328-2
; Sequence 2, Application US/10382328
; Publication No. US20030219729A1
; GENERAL INFORMATION:
; APPLICANT: YASUKAWA, Kiyoshi
; TITLE OF INVENTION: UNARY AVIAN MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS USE
; FILE REFERENCE: Q74425
; CURRENT APPLICATION NUMBER: US/10/382,328
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: JP 2002-071841
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-382-328-2

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Query Match      100.0%; Score 20; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTCTTTTATCTTCGGTTA 20
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Db 1 TTCTTTTATCTTCGGTTA 20

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RESULT 4
US-10-995-051-19
; Sequence 19, Application US/10995051
; Publication No. US20050250094A1
; GENERAL INFORMATION:
; APPLICANT: Storhoff, James
; APPLICANT: Lucas, Adam
; APPLICANT: Muller, Uwe
; APPLICANT: Bao, Yijia P

```

```

; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
; TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
; FILE REFERENCE: MBHB-03-466-E
; CURRENT APPLICATION NUMBER: US/10/995,051
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 10/854,848
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/474,569
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/499,034
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/517,450
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: 60/567,874
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 85
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNA target.
US-10-995-051-19

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Query Match      100.0%; Score 20; DB 10; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTCTTTTATCTTCGGTTA 20
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Db 36 TTCTTTTATCTTCGGTTA 55

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RESULT 5
US-10-995-051-30
; Sequence 30, Application US/10995051
; Publication No. US20050250094A1
; GENERAL INFORMATION:
; APPLICANT: Storhoff, James
; APPLICANT: Lucas, Adam
; APPLICANT: Muller, Uwe
; APPLICANT: Bao, Yijia P
; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
; TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
; FILE REFERENCE: MBHB-03-466-E
; CURRENT APPLICATION NUMBER: US/10/995,051
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 10/854,848
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/474,569
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/499,034
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/517,450
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: 60/567,874
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 86
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNA target
US-10-995-051-30

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Query Match      100.0%; Score 20; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TTCTTTTATCTTCGGTTA 20

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Db 37 TTCTTTTATCTTCGGTTA 56
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RESULT 6
US-10-995-051-14/c
; Sequence 14, Application US/10995051
; Publication No. US20050250094A1
; GENERAL INFORMATION:
; APPLICANT: Storhoff, James
; APPLICANT: Lucas, Adam
; APPLICANT: Muller, Uwe
; APPLICANT: Bao, Yijia P
; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
; TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
; FILE REFERENCE: MEHB-03-466-E
; CURRENT APPLICATION NUMBER: US/10/995,051
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 10/854,848
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/474,569
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/499,034
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/517,450
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: 60/567,874
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Target Meca 4 is a meca 281 base-pair PCR amplicon.
US-10-995-051-14

Query Match 100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
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Db 120 TTCTTTTATCTTCGGTTA 101
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RESULT 7
US-10-478-633A-151/c
; Sequence 151, Application US/10478633A
; Publication No. US2005059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 151
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-151

Query Match 100.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
|||||

Db 147 TTCTTTTATCTTCGGTTA 128
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RESULT 8
US-10-479-674-30/c
; Sequence 30, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Ruletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-30

Query Match 100.0%; Score 20; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
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Db 81 TTCTTTTATCTTCGGTTA 62
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RESULT 9
US-10-479-674-27/c
; Sequence 27, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Ruletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-27

Query Match 100.0%; Score 20; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
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Db 81 TTCTTTTATCTTCGGTTA 62
|||||

RESULT 10
US-10-479-674-29/c
; Sequence 29, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.

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/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 29
/ LENGTH: 744
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-29

Query Match      100.0%; Score 20; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.1e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
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Db 72 TTCTTTTATCTTCGGTTA 53

RESULT 11
US-10-479-674-28/c
/ Sequence 28, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 28
/ LENGTH: 782
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-28

Query Match      100.0%; Score 20; DB 9; Length 782;
Best Local Similarity 100.0%; Pred. No. 3.1e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 80 TTCTTTTATCTTCGGTTA 61

RESULT 12
US-10-479-674-191/c
/ Sequence 191, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 191
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/ LENGTH: 1858
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-191

Query Match      100.0%; Score 20; DB 9; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3.4e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 80 TTCTTTTATCTTCGGTTA 61

RESULT 13
US-10-479-674-192/c
/ Sequence 192, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 192
/ LENGTH: 1861
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-192

Query Match      100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.4e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
   |||||
Db 81 TTCTTTTATCTTCGGTTA 62

RESULT 14
US-10-479-674-193/c
/ Sequence 193, Application US/10479674
/ Publication No. US20050019893A1
/ GENERAL INFORMATION:
/ APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
/ APPLICANT: Huletsky, Ann
/ APPLICANT: Rossbach, Valery
/ TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
/ FILE REFERENCE: TV/12287.92
/ CURRENT APPLICATION NUMBER: US/10/479,674
/ CURRENT FILING DATE: 2003-12-02
/ PRIOR APPLICATION NUMBER: CA 2,348,042
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 233
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 193
/ LENGTH: 1861
/ TYPE: DNA
/ ORGANISM: Staphylococcus aureus
US-10-479-674-193

Query Match      100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.4e-02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
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Db 81 TTCTTTTATCTTCGGTTA 62

RESULT 15

US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostica (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match 100.0%; Score 20; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20

Db 1117 TTCTTTTATCTTCGGTTA 1098

Search completed: May 31, 2006, 23:02:15
Job time : 520.589 secs

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	15.8	79.0	333	7	US-11-217-529-173987	Sequence 173987, A
C 2	15.8	79.0	612	7	US-11-217-529-75910	Sequence 75910, A
C 3	15.8	79.0	1794	6	US-10-953-349-10244	Sequence 10244, A
C 4	15.8	79.0	1817	6	US-10-953-349-12711	Sequence 12711, A
C 5	15.8	79.0	2292	7	US-11-217-529-78725	Sequence 78725, A
C 6	15.8	79.0	2500	6	US-10-953-349-11714	Sequence 11714, A
C 7	15.8	79.0	2805	6	US-10-953-349-37451	Sequence 37451, A
C 8	15.8	79.0	4160	7	US-11-239-676-2	Sequence 2, Appl
C 9	15.8	79.0	135090	6	US-10-505-928-607	Sequence 607, App
C 10	15.4	77.0	2022	7	US-11-217-528-77628	Sequence 77628, A
C 11	15.2	76.0	348	7	US-11-217-529-166770	Sequence 166770, A
C 12	15.2	76.0	743	7	US-11-217-529-190895	Sequence 190895, A
C 13	15.2	76.0	1003	7	US-11-226-605-52	Sequence 52, Appl
C 14	15.2	76.0	1398	7	US-11-122-986-231	Sequence 231, App
C 15	15.2	76.0	1401	7	US-11-122-986-229	Sequence 229, App
C 16	15.2	76.0	1560	7	US-11-217-529-4485	Sequence 4485, Ap
C 17	15.2	76.0	1608	7	US-11-217-529-174404	Sequence 174404, A
C 18	15.2	76.0	1618	6	US-10-953-349-6398	Sequence 6398, Ap
C 19	15.2	76.0	1737	7	US-11-217-529-81418	Sequence 81418, A
C 20	15.2	76.0	1943	6	US-10-953-349-37312	Sequence 37312, A
C 21	15.2	76.0	2397	7	US-11-217-529-75598	Sequence 75598, A
C 22	15.2	76.0	2430	7	US-11-217-529-1233	Sequence 1233, Ap
C 23	15.2	76.0	3351	7	US-11-293-697-1390	Sequence 1390, Ap
C 24	15.2	76.0	3915	7	US-11-217-529-2644	Sequence 2644, Ap
C 25	15	75.0	9954	7	US-11-217-529-76522	Sequence 76522, A

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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75910
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (460)..(495)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-75910

Query Match          79.0%; Score 15.8; DB 7; Length 612;
Best Local Similarity 89.5%; Pred. No. 94;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      539 TTATTTTATCTTCGTGTT 521

RESULT 3
US-10-953-349-10244/c
; Sequence 10244, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10244
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10244

Query Match          79.0%; Score 15.8; DB 6; Length 1794;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      267 TTCTTTTAACTTCGTGTT 249

RESULT 4
US-10-953-349-12711
; Sequence 12711, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12711
; LENGTH: 1817
; TYPE: DNA
; ORGANISM: Glycine max

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US-10-953-349-12711
Query Match          79.0%; Score 15.8; DB 6; Length 1817;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCTTTTATCTTCGGTTA 20
Db      1704 TCTTTTATCTTCGTGTTA 1722

RESULT 5
US-11-217-529-78725/c
; Sequence 78725, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78725
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78725

Query Match          79.0%; Score 15.8; DB 7; Length 2292;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      1557 TTCTTTTATCTTCGGTT 1539

RESULT 6
US-10-953-349-11714/c
; Sequence 11714, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11714
; LENGTH: 2500
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11714

Query Match          79.0%; Score 15.8; DB 6; Length 2500;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTCTTTTATCTTCGGTT 19
Db      1894 TTCTTTTATCTTCGTGTT 1876

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RESULT 7
US-10-953-349-37451/c
; Sequence 37451, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37451
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-37451

Query Match          79.0%; Score 15.8; DB 6; Length 2805;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
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Db 494 TTCTTTTCTCTTCGATT 476

RESULT 8
US-11-239-676-2
; Sequence 2, Application US/11239676
; Publication No. US20060107348A1
; GENERAL INFORMATION:
; APPLICANT: WU, KUNSHENG
; APPLICANT: MCCLAIRD, PAUL
; APPLICANT: BYRUM, JOSEPH R.
; APPLICANT: REITER, ROBERT
; APPLICANT: ERICKSON, MARK
; TITLE OF INVENTION: HIGH YIELDING SOYBEAN PLANTS WITH LOW LINOLENIC ACID
; FILE REFERENCE: MSUT:014US
; CURRENT APPLICATION NUMBER: US/11/239,676
; CURRENT FILING DATE: 2005-09-29
; PRIOR APPLICATION NUMBER: 60/614,331
; PRIOR FILING DATE: 2004-09-29
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4160
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-239-676-2

Query Match          79.0%; Score 15.8; DB 7; Length 4160;
Best Local Similarity 89.5%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTT 19
    ||||| ||||| ||||| ||
Db 2460 TTCTTTTCTCTTCGCTT 2478

RESULT 9
US-10-505-928-607/c
; Sequence 607, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
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; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 607
; LENGTH: 135090
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-607

Query Match          79.0%; Score 15.8; DB 6; Length 135090;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCTTTTATCTTCGGTTA 20
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Db 122446 TCTTTATCTTCAGTTA 122428

RESULT 10
US-11-217-529-77628
; Sequence 77628, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77628
; LENGTH: 2022
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77628

Query Match          77.0%; Score 15.4; DB 7; Length 2022;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTTTATCTTCGGTTA 20
    ||||| ||||| ||||| ||
Db 666 TTTTCTATCTTCGGTTA 682

RESULT 11
US-11-217-529-166770/c
; Sequence 166770, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 166770
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166770

Query Match      76.0%; Score 15.2; DB 7; Length 348;
Best Local Similarity 85.0%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 282 TTCTTTTATCTTCGGTTA 263

RESULT 12
US-11-217-529-190895/c
; Sequence 190895, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190895
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190895

Query Match      76.0%; Score 15.2; DB 7; Length 743;
Best Local Similarity 85.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 674 TTCTTTTATCTTCGGTTA 655

RESULT 13
US-11-226-605-52/c
; Sequence 52, Application US/11226605
; Publication No. US20060088859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198US01
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-52

Query Match      76.0%; Score 15.2; DB 7; Length 1003;
Best Local Similarity 85.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 192 TTCTTTTATCTTCATTGA 173

RESULT 15
US-11-122-986-229/c
; Sequence 229, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 231
; LENGTH: 1398
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-11-122-986-231

Query Match      76.0%; Score 15.2; DB 7; Length 1398;
Best Local Similarity 85.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTATCTTCGGTTA 20
Db 192 TTCTTTTATCTTCATTGA 173

RESULT 15
US-11-122-986-231/c
; Sequence 229, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
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; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 229
; LENGTH: 1401
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-11-122-986-229

Query Match      76.0%; Score 15.2; DB 7; Length 1401;
Best Local Similarity 85.0%; Pred.No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TTCTTTTTCCTTCGGTTA 20
Db      192 TTCTTTTTCCTTCATTTA 173

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Search completed: May 31, 2006, 21:22:01
Job time : 7.65432 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 44.6914 Seconds
(without alignments)
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Title: US-09-865-579A-24

Perfect score: 20

Sequence: 1 tcatgtcgttaattttt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Issued Patents NA:*
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 - 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
 - 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
 - 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	20	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	20	100.0	2028	3	US-09-134-001C-1710 Sequence 1710, App
C 4	18.4	92.0	601	3	US-09-949-016-23426 Sequence 23426, A
C 5	18.4	92.0	601	3	US-09-949-016-176611 Sequence 176611, A
C 6	18.4	92.0	1133	3	US-10-000-489-57 Sequence 57, Appl
C 7	18.4	92.0	1133	4	US-09-992-095B-57 Sequence 57, Appl
C 8	18.4	92.0	1133	5	US-10-000-986A-57 Sequence 57, Appl
C 9	18.4	92.0	5372	3	US-09-949-016-5039 Sequence 5039, App
C 10	18.4	92.0	5387	3	US-09-949-016-265 Sequence 265, App
C 11	18.4	92.0	55703	3	US-09-949-016-12007 Sequence 12007, A
C 12	18.4	92.0	55703	3	US-09-949-016-16781 Sequence 16781, A
C 13	18	90.0	27	2	US-08-743-637B-262 Sequence 262, App
C 14	17.4	87.0	94077	3	US-09-949-016-13635 Sequence 13635, A
C 15	17.4	87.0	264358	3	US-09-949-016-15725 Sequence 15725, A
C 16	17	85.0	330	2	US-08-437-013-4 Sequence 4, Appli
C 17	17	85.0	330	3	US-09-275-506A-4 Sequence 4, Appli
C 18	17	85.0	601	3	US-09-949-016-69828 Sequence 69828, A
C 19	17	85.0	601	3	US-09-949-016-69829 Sequence 69829, A
C 20	17	85.0	601	3	US-09-949-016-96132 Sequence 96132, A
C 21	17	85.0	601	3	US-09-949-016-96133 Sequence 96133, A
C 22	17	85.0	641	2	US-08-437-013-1 Sequence 1, Appli
C 23	17	85.0	641	2	US-08-437-013-28 Sequence 28, Appli

24	17	85.0	641	3	US-09-275-506A-1	Sequence 1, Appli
25	17	85.0	641	3	US-09-275-506A-28	Sequence 28, Appl
26	17	85.0	700	3	US-09-735-271-332	Sequence 332, App
27	17	85.0	700	3	US-09-735-271-333	Sequence 333, App
28	17	85.0	709	2	US-08-437-013-26	Sequence 26, Appl
29	17	85.0	709	3	US-09-275-506A-26	Sequence 26, Appl
C 30	17	85.0	12690	3	US-09-949-016-13799	Sequence 13799, A
31	17	85.0	387902	3	US-09-949-016-14543	Sequence 14543, A
32	17	85.0	421883	3	US-09-949-016-12557	Sequence 12557, A
33	16.8	84.0	497	3	US-09-621-976-2000	Sequence 2000, Ap
34	16.8	84.0	601	3	US-09-949-016-67918	Sequence 67918, A
C 35	16.8	84.0	601	3	US-09-949-016-81047	Sequence 81047, A
36	16.8	84.0	601	3	US-09-949-016-156906	Sequence 156906, A
37	16.8	84.0	601	3	US-09-949-016-156907	Sequence 156907, A
38	16.8	84.0	601	3	US-09-949-016-166158	Sequence 166158, A
C 39	16.8	84.0	601	3	US-09-949-016-173357	Sequence 173357, A
C 40	16.8	84.0	601	3	US-09-949-016-173358	Sequence 173358, A
41	16.8	84.0	805	2	US-08-118-469A-6	Sequence 6, Appli
42	16.8	84.0	805	2	US-08-909-119-6	Sequence 6, Appli
43	16.8	84.0	805	3	US-09-152-588-6	Sequence 6, Appli
44	16.8	84.0	2119	3	US-09-240-639-7	Sequence 7, Appli
45	16.8	84.0	2119	3	US-09-908-510A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match      100.0%; Score 20; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
    |||||
Db 1234 TCATTGCTGTTAATATTTT 1215

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
    |||||
Db 1234 TCATTGCTGTTAATATTTT 1215

RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
```

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; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 20; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
    |||||
Db 1255 TCATTGCTGTTAATATTTT 1236

RESULT 4
US-09-949-016-23426/c
; Sequence 23426, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23426
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23426

Query Match      92.0%; Score 18.4; DB 3; Length 601;
Best Local Similarity 95.0%; Pred. No. 83;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20
    |||||
Db 284 TAATTGCTGTTAATATTTT 265

RESULT 5
US-09-949-016-176611/c
; Sequence 176611, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 176611
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-176611

Query Match 92.0%; Score 18.4; DB 3; Length 601;
 Best Local Similarity 95.0%; Pred. No. 83;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATATTTTT 20
 Db 284 TAATTGCTGTTAATATTTTT 265

RESULT 6

US-10-000-489-57
 ; Sequence 57, Application US/10000489
 ; Patent No. 6794363
 ; GENERAL INFORMATION:
 ; APPLICANT: Benjanin, Stephane
 ; APPLICANT: Tanaka, Hiroaki
 ; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 91.US6.DIV
 ; CURRENT APPLICATION NUMBER: US/10/000,489
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: US 09/924,340
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01715
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 60/305,456
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/302,277
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 60/298,698
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: US 60/293,574
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: JPatent
 ; SEQ ID NO 57
 ; LENGTH: 1133
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1..475
 ; NAME/KEY: CDS
 ; LOCATION: 476..964
 ; NAME/KEY: 3'UTR
 ; LOCATION: 965..1133
 ; NAME/KEY: polyA signal
 ; LOCATION: 1101..1106
 ; NAME/KEY: polyA site
 ; LOCATION: 1118..1133

Query Match 92.0%; Score 18.4; DB 3; Length 1133;
 Best Local Similarity 95.0%; Pred. No. 85;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATATTTTT 20

Db 1076 TAATTGCTGTTAATATTTTT 1095

RESULT 7

US-09-992-095B-57
 ; Sequence 57, Application US/09992095B
 ; Patent No. 6989262
 ; GENERAL INFORMATION:
 ; APPLICANT: Benjanin, Stephane
 ; APPLICANT: Tanaka, Hiroaki
 ; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 91.US5.DIV
 ; CURRENT APPLICATION NUMBER: US/09/992,095B
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: US 09/924,340
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01715
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 60/305,456
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/302,277
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR APPLICATION NUMBER: US 60/298,698
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: US 60/293,574
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: JPatent
 ; SEQ ID NO 57
 ; LENGTH: 1133
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1..475
 ; NAME/KEY: CDS
 ; LOCATION: 476..964
 ; NAME/KEY: 3'UTR
 ; LOCATION: 965..1133
 ; NAME/KEY: polyA signal
 ; LOCATION: 1101..1106
 ; NAME/KEY: polyA site
 ; LOCATION: 1118..1133

Query Match 92.0%; Score 18.4; DB 4; Length 1133;
 Best Local Similarity 95.0%; Pred. No. 85;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCATTGCTGTTAATATTTTT 20
 Db 1076 TAATTGCTGTTAATATTTTT 1095

RESULT 8

US-10-000-986A-57
 ; Sequence 57, Application US/10000986A
 ; Patent No. 7005500
 ; GENERAL INFORMATION:
 ; APPLICANT: Benjanin, Stephane
 ; APPLICANT: Tanaka, Hiroaki
 ; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
 ; FILE REFERENCE: G-091US09DIV
 ; CURRENT APPLICATION NUMBER: US/10/000,986A
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: US 09/924,340
 ; PRIOR FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: PCT/IB01/01715

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/ PRIOR FILING DATE: 2001-08-06
/ PRIOR APPLICATION NUMBER: US 60/305,456
/ PRIOR FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: US 60/302,277
/ PRIOR FILING DATE: 2001-06-29
/ PRIOR APPLICATION NUMBER: US 60/298,698
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: US 60/293,574
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: Jpatent
/ SEQ ID NO 57
/ LENGTH: 1133
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..475
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 476..964
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: 965..1133
/ FEATURE:
/ NAME/KEY: polyA signal
/ LOCATION: 1101..1106
/ FEATURE:
/ NAME/KEY: polyA site
/ LOCATION: 1118..1133
/ LOCATION: 1118..1133
US-10-000-986A-57

Query Match          92.0%; Score 18.4; DB 5; Length 1133;
Best Local Similarity 95.0%; Pred. No. 85;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1076 TAATTGCTGTTAAATATTTT 1095

RESULT 9
US-09-949-016-5039
/ Sequence 5039, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5039
/ LENGTH: 5372
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-5039

Query Match          92.0%; Score 18.4; DB 3; Length 5372;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 5077 TAATTGCTGTTAAATATTTT 5096

RESULT 10
US-09-949-016-265
/ Sequence 265, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 265
/ LENGTH: 5387
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-265

Query Match          92.0%; Score 18.4; DB 3; Length 5387;
Best Local Similarity 95.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 5075 TAATTGCTGTTAAATATTTT 5094

RESULT 11
US-09-949-016-12007
/ Sequence 12007, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12007
/ LENGTH: 55703
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-12007

Query Match          92.0%; Score 18.4; DB 3; Length 55703;
Best Local Similarity 95.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 53408 TAATTGCTGTTAAATATTTT 53427

RESULT 12
US-09-949-016-16781
/ Sequence 16781, Application US/09949016
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16781
; LENGTH: 55703
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-16781

Query Match          92.0%; Score 18.4; DB 3; Length 55703;
Best Local Similarity 95.0%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCATTCGCTGTTAATATTTT 20
      |||||||
Db      53408 TAATGCTGTTAATATTTT 53427

RESULT 13
US-08-743-637B-262
; Sequence 262, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 262:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-743-637B-262

Query Match          90.0%; Score 18; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 ATTGCTGTTAATATTTT 20
      |||||||
Db      1 ATTGCTGTTAATATTTT 18

RESULT 14
US-09-949-016-13635
; Sequence 13635, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13635
; LENGTH: 94077
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13635

Query Match          87.0%; Score 17.4; DB 3; Length 94077;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CATTCGCTGTTAATATTTT 20
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Db      72712 CATTCGCTGTTAATATTTT 72730

RESULT 15
US-09-949-016-15725/c
; Sequence 15725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15725
; LENGTH: 264358
; TYPE: DNA
; ORGANISM: Human
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (264358)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15725

Query Match      87.0%; Score 17.4; DB 3; Length 264358;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAAATATTTT 19
Db      115919 TCATTGCTGTTAAATATTTT 115901

Search completed: May 31, 2006, 21:13:03
Job time : 45.6914 secs
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 519.589 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-24

Perfect score: 20

Sequence: 1 tcattgctgtaataattttt 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	3	US-09-865-579A-14
2	20	100.0	20	3	US-09-865-579A-24
3	20	100.0	281	10	US-10-995-051-14
4	20	100.0	560	10	US-10-478-633A-151
5	20	100.0	652	9	US-10-479-674-30
6	20	100.0	657	9	US-10-479-674-27
7	20	100.0	744	9	US-10-479-674-29
8	20	100.0	782	9	US-10-479-674-28
9	20	100.0	1858	9	US-10-479-674-191
10	20	100.0	1861	9	US-10-479-674-192
11	20	100.0	1861	9	US-10-479-674-193
12	20	100.0	1957	9	US-10-479-674-82
13	20	100.0	2007	7	US-09-452-599-169
14	20	100.0	2007	7	US-10-121-120-169
15	20	100.0	2007	9	US-10-479-674-78
16	20	100.0	2007	9	US-10-479-674-90
17	20	100.0	2007	9	US-10-479-674-91

C 18	20	100.0	2007	9	US-10-121-120-169	Sequence 169, App
C 19	20	100.0	2028	8	US-10-724-972A-3141	Sequence 3141, App
C 20	20	100.0	2386	9	US-10-479-674-224	Sequence 224, App
C 21	20	100.0	2410	9	US-10-479-674-190	Sequence 190, App
C 22	20	100.0	2436	9	US-10-479-674-31	Sequence 31, App
C 23	20	100.0	3101	9	US-10-479-674-195	Sequence 195, App
C 24	20	100.0	3506	9	US-10-479-674-196	Sequence 196, App
C 25	18.4	92.0	366	4	US-09-925-065A-405159	Sequence 405159, App
C 26	18.4	92.0	366	5	US-09-925-065A-405159	Sequence 405159, App
C 27	18.4	92.0	648	6	US-10-001-843-114	Sequence 114, App
C 28	18.4	92.0	648	13	US-11-005-609-114	Sequence 114, App
C 29	18.4	92.0	928	6	US-10-001-843-115	Sequence 115, App
C 30	18.4	92.0	928	13	US-11-005-609-115	Sequence 115, App
C 31	18.4	92.0	1133	3	US-09-992-600A-57	Sequence 57, App
C 32	18.4	92.0	1133	3	US-09-924-340-57	Sequence 57, App
C 33	18.4	92.0	1133	3	US-09-992-095B-57	Sequence 57, App
C 34	18.4	92.0	1133	3	US-09-999-570-57	Sequence 57, App
C 35	18.4	92.0	1133	6	US-10-000-489-57	Sequence 57, App
C 36	18.4	92.0	1133	6	US-10-000-986-57	Sequence 57, App
C 37	18.4	92.0	1133	7	US-10-154-678-57	Sequence 57, App
C 38	18.4	92.0	1133	7	US-10-001-142-57	Sequence 57, App
C 39	18.4	92.0	1133	9	US-10-838-854-57	Sequence 57, App
C 40	18.4	92.0	1177	6	US-10-027-632-9829	Sequence 9829, App
C 41	18.4	92.0	1177	6	US-10-027-632-30498	Sequence 30498, App
C 42	18.4	92.0	1177	6	US-10-027-632-30499	Sequence 30499, App
C 43	18.4	92.0	1177	7	US-10-027-632-9829	Sequence 9829, App
C 44	18.4	92.0	1177	7	US-10-027-632-30498	Sequence 30498, App
C 45	18.4	92.0	1177	7	US-10-027-632-30499	Sequence 30499, App

ALIGNMENTS

RESULT 1

US-09-865-579A-14
; Sequence 14, Application US/09865579A
; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATATTTT 20

Db 1 TCATTGCTGTTAATATTTT 20

RESULT 2

US-09-865-579A-24
; Sequence 24, Application US/09865579A

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; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-865-579A-24

Query Match      100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||
DB 1 TCATTGCTGTTAAATATTTT 20

RESULT 3
US-10-995-051-14/c
; Sequence 14, Application US/10995051
; Publication No. US20050250094A1
; GENERAL INFORMATION:
; APPLICANT: Storchoff, James
; APPLICANT: Lucas, Adam
; APPLICANT: Muller, Uwe
; APPLICANT: Bao, Yijia P
; TITLE OF INVENTION: Method for Detecting Analytes Based on Evanescent Illumination
; TITLE OF INVENTION: and Scatter-Based Detection of Nanoparticle Probe Complexes
; FILE REFERENCE: MBHB-03-466-E
; CURRENT APPLICATION NUMBER: US/10/995,051
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 10/854,848
; PRIOR FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: 60/474,569
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: 60/499,034
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 60/517,450
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: 60/567,874
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 281
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Target MecA 4 is a mecA 281 base-pair PCR amplicon.
US-10-995-051-14

Query Match      100.0%; Score 20; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
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DB 187 TCATTGCTGTTAAATATTTT 168

RESULT 4
US-10-478-633A-151/c
; Sequence 151, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent f
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 151
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-151

Query Match      100.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||
DB 214 TCATTGCTGTTAAATATTTT 195

RESULT 5
US-10-479-674-30/c
; Sequence 30, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIST
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 652
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-30

Query Match      100.0%; Score 20; DB 9; Length 652;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
    |||||||
DB 148 TCATTGCTGTTAAATATTTT 129

RESULT 6
US-10-479-674-27/c
; Sequence 27, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rossbach, Valery

```

```
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-27

Query Match      100.0%; Score 20; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
      |||||||
Db      148 TCATTGCTGTTAATATTTT 129

RESULT 7
US-10-479-674-29/c
; Sequence 29, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-29

Query Match      100.0%; Score 20; DB 9; Length 744;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
      |||||||
Db      139 TCATTGCTGTTAATATTTT 120

RESULT 8
US-10-479-674-28/c
; Sequence 28, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 782
; TYPE: DNA
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; ORGANISM: Staphylococcus aureus
US-10-479-674-28

Query Match      100.0%; Score 20; DB 9; Length 782;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
      |||||||
Db      147 TCATTGCTGTTAATATTTT 128

RESULT 9
US-10-479-674-191/c
; Sequence 191, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 191
; LENGTH: 1858
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-191

Query Match      100.0%; Score 20; DB 9; Length 1858;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
      |||||||
Db      147 TCATTGCTGTTAATATTTT 128

RESULT 10
US-10-479-674-192/c
; Sequence 192, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-192

Query Match      100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAATATTTT 20
      |||||||
Db      148 TCATTGCTGTTAATATTTT 129
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RESULT 11
US-10-479-674-193/c
; Sequence 193, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 193
; LENGTH: 1861
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-193

Query Match      100.0%; Score 20; DB 9; Length 1861;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATTTTT 20
DB 148 TCATTGCTGTTAATAATTTTT 129

RESULT 12
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 20; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATTTTT 20
DB 1184 TCATTGCTGTTAATAATTTTT 1165

RESULT 13
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US2002005101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
```

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; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 20; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATTTTT 20
DB 1234 TCATTGCTGTTAATAATTTTT 1215

RESULT 14
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US2003018073A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Sequences for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 20; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAATAATTTTT 20
DB 1234 TCATTGCTGTTAATAATTTTT 1215

RESULT 15
US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
; FILE REFERENCE: TV/12287.92
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; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

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Query Match      100.0%; Score 20; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 TCATTGCTGTTAATATTTT 20
        |||||||
Db      1234 TCATTGCTGTTAATATTTT 1215

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Search completed: May 31, 2006, 23:02:17
Job time : 519.589 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 7.65432 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-24
Perfect score: 20
Sequence: 1 tcattgctgtaataattttt 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA New:
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB_seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB_seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB_seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB_seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	16.8	84.0	555	7	US-11-217-529-174434 Sequence 174434, App
C 3	16.8	84.0	1728	7	US-11-217-529-1190 Sequence 1190, App
C 4	16.8	84.0	2163	7	US-11-217-529-78062 Sequence 78062, A
C 5	16.8	84.0	2370	7	US-11-217-529-1315 Sequence 1315, App
C 6	16.8	84.0	3891	7	US-11-217-529-1874 Sequence 1874, App
C 7	15.8	79.0	2411	7	US-11-293-697-994 Sequence 994, App
C 8	15.8	79.0	5003	6	US-10-473-173-112 Sequence 112, App
C 9	15.8	79.0	394191	6	US-10-506-549-3 Sequence 3, Appli
C 10	15.4	77.0	444	7	US-11-328-747-3 Sequence 3, Appli
C 11	15.4	77.0	885	7	US-11-217-529-3736 Sequence 3736, App
C 12	15.4	77.0	2082	7	US-11-293-697-698 Sequence 698, App
C 13	15.4	77.0	3547	7	US-11-293-697-1247 Sequence 1247, App
C 14	15.2	76.0	1101	7	US-11-217-529-75496 Sequence 75496, A
C 15	15.2	76.0	1122	7	US-11-217-529-78201 Sequence 78201, A
C 16	15.2	76.0	1124	6	US-10-953-349-7279 Sequence 7279, App
C 17	15.2	76.0	1308	6	US-10-504-120-14 Sequence 14, Appli
C 18	15.2	76.0	1488	7	US-11-217-529-79270 Sequence 79270, A
C 19	15.2	76.0	1536	7	US-11-217-529-76326 Sequence 76326, A
C 20	15.2	76.0	1566	7	US-11-217-529-79711 Sequence 79711, A
C 21	15.2	76.0	1827	7	US-11-217-529-82557 Sequence 82557, A
C 22	15.2	76.0	1938	7	US-11-217-529-3079 Sequence 3079, App
C 23	15.2	76.0	2127	7	US-11-217-529-2653 Sequence 2653, App
C 24	15.2	76.0	2370	7	US-11-217-529-77236 Sequence 77236, A
C 25	15.2	76.0	3190	7	US-11-293-697-323 Sequence 323, App

C 26	15.2	76.0	3675	7	US-11-217-529-79669 Sequence 79669, A
C 27	15.2	76.0	3756	7	US-11-217-529-77878 Sequence 77878, A
C 28	15.2	76.0	3915	7	US-11-217-529-4858 Sequence 4858, App
C 29	15.2	76.0	4218	7	US-11-217-529-75740 Sequence 75740, A
C 30	15	75.0	1340	6	US-10-953-349-2052 Sequence 2052, App
C 31	14.8	74.0	460	7	US-11-134-445-4 Sequence 4, Appli
C 32	14.8	74.0	462	7	US-11-134-445-42 Sequence 42, Appli
C 33	14.8	74.0	1233	7	US-11-217-529-76781 Sequence 76781, A
C 34	14.8	74.0	1242	7	US-11-217-529-80870 Sequence 80870, A
C 35	14.8	74.0	1359	7	US-11-217-529-75588 Sequence 75588, A
C 36	14.8	74.0	1404	7	US-11-217-529-190888 Sequence 190888, A
C 37	14.8	74.0	1564	6	US-10-953-349-4201 Sequence 4201, App
C 38	14.8	74.0	1611	7	US-11-217-529-2851 Sequence 2851, App
C 39	14.8	74.0	2286	7	US-11-293-697-230 Sequence 230, App
C 40	14.8	74.0	2660	7	US-11-293-697-801 Sequence 801, App
C 41	14.8	74.0	3054	6	US-10-528-032-12 Sequence 12, Appli
C 42	14.8	74.0	6809	6	US-10-713-648A-24 Sequence 24, Appli
C 43	14.8	74.0	70665	6	US-10-505-928-596 Sequence 596, App
C 44	14.8	74.0	394191	6	US-10-506-549-3 Sequence 3, Appli
C 45	14.4	72.0	1140	7	US-11-217-529-6176 Sequence 6176, App

ALIGNMENTS

RESULT 1
US-11-217-529-286/c
; Sequence 286, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 286
; LENGTH: 4881
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-286

Query Match 87.0%; Score 17.4; DB 7; Length 4881;
Best Local Similarity 94.7%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CATTGCTGTTAATATTTT 20
DB 4702 CATTGCTGTTAATATTTT 4684

RESULT 2
US-11-217-529-174434/c
; Sequence 174434, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17434
; LENGTH: 555
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-17434

Query Match      84.0%; Score 16.8; DB 7; Length 555;
Best Local Similarity 90.0%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 338 TCATTGTTGTTAAATATT 319

RESULT 3
US-11-217-529-1190/c
; Sequence 1190, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1190
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1190

Query Match      84.0%; Score 16.8; DB 7; Length 1728;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1016 TCATTGATGTTAAATATTTT 997

RESULT 4
US-11-217-529-78062/c
; Sequence 78062, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1190
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1190

Query Match      84.0%; Score 16.8; DB 7; Length 1728;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1016 TCATTGATGTTAAATATTTT 997

RESULT 5
US-11-217-529-1315/c
; Sequence 1315, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1315
; LENGTH: 2370
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1315

Query Match      84.0%; Score 16.8; DB 7; Length 2370;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1504 TCATTGCTGTTACTATTTCT 1485

RESULT 6
US-11-217-529-1874/c
; Sequence 1874, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1874
; LENGTH: 3891
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1874

Query Match      84.0%; Score 16.8; DB 7; Length 2370;
Best Local Similarity 90.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCATTGCTGTTAAATATTTT 20
Db 1504 TCATTGCTGTTACTATTTCT 1485

RESULT 7
US-11-217-529-1874/c
; Sequence 1874, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1874
; LENGTH: 3891
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1874
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RESULT 9
US-10-506-549-3
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1

RESULT 11
US-11-217-529-3736/c
; Sequence 3736, Application US/11217529

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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3736
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3736

Query Match      77.0%; Score 15.4; DB 7; Length 885;
Best Local Similarity 94.1%; Pred. No. 98;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 TTGCTGTTAAATATTTT 20
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DB      164 TTGCTGTTAAATATTTT 148

RESULT 12
US-11-293-697-698
; Sequence 698, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; PRIOR FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 698
; LENGTH: 2082
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-698

Query Match      77.0%; Score 15.4; DB 7; Length 2082;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ATTGCTGTTAAATATTTT 19
        |||||
DB      1746 ATTGCTGTTAAATATTTT 1762

RESULT 13
US-11-293-697-1247
; Sequence 1247, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; ORGANISM: Saccharomyces pastorianus

US-11-217-529-75496/c
; Sequence 75496, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75496
; LENGTH: 1101
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75496

Query Match      76.0%; Score 15.2; DB 7; Length 1101;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TCATTGCTGTTAAATATTTT 20
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DB      542 TCATTGCTGTTGACATATT 523

RESULT 15
US-11-217-529-78201/c
; Sequence 78201, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78201
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
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US-11-217-529-78201

Query Match 76.0%; Score 15.2; DB 7; Length 1122;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db	197	TCATTGCTATTATTAATT	178

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 62.5679 Seconds
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Title: US-09-865-579A-25
Perfect score: 28
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- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	28	100.0	2007	2	US-08-743-637B-169
3	28	100.0	2007	3	US-08-526-840B-169
4	28	100.0	2028	3	US-09-134-001C-1710
5	25	89.3	89	3	US-09-109-329-4
6	20.6	73.6	270	3	US-09-107-433-379
7	20.6	73.6	13206	3	US-08-961-527-33
8	20.6	73.6	16995	3	US-08-961-527-82
9	20	71.4	106450	3	US-09-949-016-13873
10	19.2	68.6	516	3	US-09-621-976-2388
11	19	67.9	192	3	US-09-107-433-313
12	19	67.9	270	3	US-09-107-433-311
13	19	67.9	276	3	US-09-583-110-345
14	19	67.9	300	3	US-09-107-433-988
15	19	67.9	537	3	US-09-583-110-1340
16	19	67.9	573	3	US-09-583-110-19
17	19	67.9	573	3	US-09-583-110-598
18	19	67.9	573	3	US-09-583-110-599
19	19	67.9	573	3	US-09-583-110-620
20	19	67.9	573	3	US-09-583-110-1285
21	19	67.9	573	3	US-09-583-110-2541
22	19	67.9	573	3	US-09-107-433-312
23	19	67.9	597	3	US-09-107-433-1465

c	24	19	67.9	747	3	US-09-601-198-138	Sequence 138, App
c	25	19	67.9	1305	3	US-09-543-681A-2094	Sequence 2094, Ap
c	26	19	67.9	1635	3	US-09-601-198-10	Sequence 10, Appl
c	27	19	67.9	2996	3	US-08-961-527-260	Sequence 260, App
c	28	19	67.9	11309	3	US-08-961-527-108	Sequence 108, App
c	29	19	67.9	134499	4	US-09-531-120-192	Sequence 192, App
c	30	18.6	66.4	226	3	US-09-235-451-40	Sequence 40, Appl
c	31	18.6	66.4	226	3	US-09-978-303-40	Sequence 40, Appl
c	32	18.6	66.4	11443	3	US-08-961-527-49	Sequence 49, Appl
c	33	18.6	66.4	51336	3	US-09-949-016-16054	Sequence 16054, A
c	34	18.4	65.7	468	3	US-09-543-681A-1990	Sequence 1990, Ap
c	35	18.4	65.7	601	3	US-09-949-016-195930	Sequence 195930, A
c	36	18.4	65.7	741	3	US-09-328-352-2187	Sequence 2187, Ap
c	37	18.4	65.7	903	3	US-09-248-796A-254	Sequence 254, App
c	38	18.4	65.7	147321	3	US-09-949-016-15450	Sequence 15450, A
c	39	18.4	65.7	251672	3	US-09-949-016-17296	Sequence 17296, A
c	40	18.4	65.7	251682	3	US-09-949-016-11973	Sequence 11973, A
c	41	18.2	65.0	601	3	US-09-949-016-42368	Sequence 42368, A
c	42	18.2	65.0	601	3	US-09-949-016-42369	Sequence 42369, A
c	43	18.2	65.0	11811	3	US-09-949-016-15776	Sequence 15776, A
c	44	18.2	65.0	18122	3	US-09-949-016-12956	Sequence 12956, A
c	45	18.2	65.0	237241	3	US-09-949-016-16101	Sequence 16101, A

ALIGNMENTS

RESULT 1
US-09-109-329-13
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA gene from Staphylococcal Species

US-09-109-329-13

Query Match 100.0%; Score 28; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACAACTATTGATGCTAAAGTCAAA 28
|||
Db 67 CAACAACTATTGATGCTAAAGTCAAA 94

RESULT 2

US-08-743-637B-169
; Sequence 169, Application US/08743637B
; Patent No. 5994066

GENERAL INFORMATION:
APPLICANT: BERGERON, Michel G.
APPLICANT: PICARD, Francois J.
APPLICANT: OUELLETTE, Marc
APPLICANT: ROY, Paul H.

TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...

```
;
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-743-637B-169

Query Match 100.0%; Score 28; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACAACTATTGATGCTAAAGTTCAAA 1000

RESULT 3
US-08-526-840B-169
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
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;
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-526-840B-169

Query Match 100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAACTATTGATGCTAAAGTTCAAA 28
Db 973 CAACAACTATTGATGCTAAAGTTCAAA 1000

RESULT 4
US-09-134-001C-1710
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
; US-09-134-001C-1710

Query Match 100.0%; Score 28; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAACTATTGATGCTAAAGTTCAAA 28
Db 994 CAACAACTATTGATGCTAAAGTTCAAA 1021

RESULT 5
US-09-109-329-4/c
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; TITLE OF INVENTION: STAPHYLOCOCCI
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; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match      89.3%; Score 25; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACAACTATTGATGCTAAAGTTC 25
   |||||
Db 25 CAACAACTATTGATGCTAAAGTTC 1

RESULT 6
US-09-107-433-379
; Sequence 379, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTIC
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
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; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1....270
; SEQUENCE DESCRIPTION: SEQ ID NO: 379:
US-09-107-433-379

Query Match      73.6%; Score 20.6; DB 3; Length 270;
Best Local Similarity 85.2%; Pred. No. 16;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
Db 62 AACTAACTATTGATGATAAAGTTCAGA 88
   |||||

RESULT 7
US-08-961-527-33/c
; Sequence 33, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-33

Query Match      73.6%; Score 20.6; DB 3; Length 13206;
Best Local Similarity 85.2%; Pred. No. 22;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
Db 777 AACTAACTATTGATGATAAAGTTCAGA 751
   |||||

RESULT 8
US-08-961-527-82/c
; Sequence 82, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16995 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-961-527-82

Query Match 73.6%; Score 20.6; DB 3; Length 16995;
Best Local Similarity 85.2%; Pred. No. 23;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAATTATGCTGCTAAAGTTCAA 28
DB 456 AACTAATTATGCTGCTAAAGTTCAA 430

RESULT 9
US-09-949-016-13873/c
; Sequence 13873, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13873
; LENGTH: 106450
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13873

Query Match 71.4%; Score 20; DB 3; Length 106450;
Best Local Similarity 82.1%; Pred. No. 48;
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAACTAATTATGCTGCTAAAGTTCAA 28

DB 71484 CTACTAAGTGTGCTGCTAAATTCAAA 71457

RESULT 10
US-09-621-976-2388
; Sequence 2388, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2388
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 78..308
; US-09-621-976-2388

Query Match 68.6%; Score 19.2; DB 3; Length 516;
Best Local Similarity 87.5%; Pred. No. 66;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CTAACATTTGCTGCTAAAGTTCAA 27
DB 347 CTAACATTTGCTGCTAAAGTTGAA 370

RESULT 11
US-09-107-433-313
; Sequence 313, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A. Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277

Job time : 63.5679 secs

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998

APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-011

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 988:

SEQUENCE CHARACTERISTICS:

LENGTH: 300 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...300

SEQUENCE DESCRIPTION: SEQ ID NO: 988:

US-09-107-433-988

Query Match 67.9%; Score 19; DB 3; Length 300;

Best Local Similarity 81.5%; Pred. No. 77;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTAACTATTGATGCTAAAGTTCAAA 28

Db 92 AATTAACCTATGATGATAAAGTTCAGA 118

RESULT 15

US-09-583-110-1340

; Sequence 1340, Application US/09583110

; Patent No. 6699703

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.

; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

; FILE REFERENCE: PATH00-07A

; CURRENT APPLICATION NUMBER: US/09/583,110

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/107,433

; PRIOR FILING DATE: 1998-06-30

; PRIOR APPLICATION NUMBER: US 60/085,131

; PRIOR FILING DATE: 1998-05-12

; PRIOR APPLICATION NUMBER: US 60/051,553

; PRIOR FILING DATE: 1997-07-02

; NUMBER OF SEQ ID NOS: 5322

; SEQ ID NO 1340

; LENGTH: 537

; TYPE: DNA

; ORGANISM: Streptococcus pneumoniae

US-09-583-110-1340

Query Match 67.9%; Score 19; DB 3; Length 537;

Best Local Similarity 81.5%; Pred. No. 81;

Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTAACTATTGATGCTAAAGTTCAAA 28

Db 5 AATTAACCTATGATGATAAAGTTCAGA 31

Search completed: May 31, 2006, 21:13:05

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 727.424 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-25

Perfect score: 28

Sequence: 1 caactaactattgatgctaaagtccaaa 28

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	28	3	US-09-865-579A-25
2	28	100.0	28	7	Sequence 25, Appl
3	28	100.0	28	3	Sequence 1, Appl
4	28	100.0	1957	3	US-10-382-328-1
5	28	100.0	2007	3	US-10-479-674-82
6	28	100.0	2007	3	US-09-452-599-169
7	28	100.0	2007	7	US-10-121-120-169
8	28	100.0	2007	9	US-10-479-674-78
9	28	100.0	2007	9	US-10-479-674-90
10	28	100.0	2007	9	US-10-479-674-91
11	22.2	79.3	1163020	8	US-10-724-972A-3141
12	22.2	79.3	3011208	8	US-10-398-221-10
13	20.6	73.6	252	9	Sequence 2058, Ap
14	20.6	73.6	270	10	Sequence 4935, Ap
15	20.6	73.6	507	9	US-10-472-928-4935
16	20.6	73.6	13206	2	US-10-617-320-379
17	20.6	73.6	13206	8	US-10-472-928-625
					Sequence 379, App
					Sequence 625, App
					Sequence 33, Appl
					Sequence 33, Appl

C 18	20.6	73.6	16995	2	US-08-961-527-82	Sequence 82, Appl
C 19	20.6	73.6	16995	8	US-10-158-844-82	Sequence 82, Appl
C 20	20.6	73.6	2162598	9	US-10-472-928-4939	Sequence 4939, Ap
C 21	20.2	72.1	477	8	US-10-424-599-78315	Sequence 78315, A
C 22	20	71.4	522	12	US-10-301-480-72989	Sequence 72989, A
C 23	20	71.4	522	12	US-10-301-480-686398	Sequence 686398, A
C 24	20	71.4	546	6	US-10-027-632-231114	Sequence 231114,
C 25	20	71.4	546	6	US-10-027-632-231115	Sequence 231115,
C 26	20	71.4	546	7	US-10-027-632-231114	Sequence 231114,
C 27	20	71.4	546	7	US-10-027-632-231115	Sequence 231115,
C 28	20	71.4	612	5	US-09-925-065A-900768	Sequence 900768,
C 29	20	71.4	612	5	US-09-925-065A-900768	Sequence 900768,
C 30	20	71.4	644	4	US-09-925-065A-904307	Sequence 904307,
C 31	20	71.4	644	5	US-09-925-065A-904307	Sequence 904307,
C 32	19.6	70.0	532	12	US-10-301-480-268574	Sequence 268574,
C 33	19.6	70.0	532	12	US-10-301-480-268574	Sequence 268574,
C 34	19.6	70.0	538	4	US-09-925-065A-177463	Sequence 177463,
C 35	19.6	70.0	538	5	US-09-925-065A-177463	Sequence 177463,
C 36	19.6	70.0	577	4	US-09-925-065A-177464	Sequence 177464,
C 37	19.6	70.0	577	5	US-09-925-065A-177464	Sequence 177464,
C 38	19.6	70.0	588	12	US-10-301-480-268575	Sequence 268575,
C 39	19.6	70.0	588	12	US-10-301-480-268575	Sequence 268575,
C 40	19.2	68.6	491	3	US-09-560-863-992	Sequence 881984,
C 41	19.2	68.6	532	4	US-09-925-065A-844656	Sequence 992, App
C 42	19.2	68.6	532	5	US-09-925-065A-844656	Sequence 844656,
C 43	19	67.9	192	10	US-10-617-320-313	Sequence 313, App
C 44	19	67.9	270	10	US-10-617-320-311	Sequence 311, App
C 45	19	67.9	300	10	US-10-617-320-988	Sequence 988, App

ALIGNMENTS

RESULT 1

US-09-865-579A-25

; Sequence 25, Application US/09865579A

; Patent No. US20020098492A1

; GENERAL INFORMATION:

; APPLICANT: Taya, Toshiki

; APPLICANT: Ishiguro, Takahiko

; APPLICANT: Saito, Juichi

; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of

; FILE REFERENCE: 9558-003-27

; CURRENT APPLICATION NUMBER: US/09/865,579A

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: JP 2000-163149

; PRIOR FILING DATE: 2000-05-29

; PRIOR APPLICATION NUMBER: JP 2000-179394

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 28

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-09-865-579A-25

Query Match 100.0%; Score 28; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

QY 1 CAACAACTATTGATGCTAAAGTTCAAA 28

Db 1 CAACAACTATTGATGCTAAAGTTCAAA 28

RESULT 2

US-10-382-328-1

; Sequence 1, Application US/10382328

; Publication No. US20030219729A1

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; GENERAL INFORMATION:
; APPLICANT: YASUKAWA, Kiyoshi
; TITLE OF INVENTION: UNARY AVIAN MYELOBLASTOSIS VIRUS REVERS TRANSCRIPTASE AND ITS USE
; FILE REFERENCE: Q74425
; CURRENT APPLICATION NUMBER: US/10/382,328
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: JP 2002-071841
; PRIOR FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-382-328-1

Query Match      100.0%; Score 28; DB 7; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
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Db 1 CAACTAACTATTGATGCTAAAGTTCAAA 28

RESULT 3
US-10-479-674-82
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      100.0%; Score 28; DB 9; Length 1957;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
Db 923 CAACTAACTATTGATGCTAAAGTTCAAA 950

RESULT 4
US-09-452-599-169
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
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; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match      100.0%; Score 28; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
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Db 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 5
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAAA 28
   |||||
Db 973 CAACTAACTATTGATGCTAAAGTTCAAA 1000

RESULT 6
US-10-479-674-78
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosbach, Valery
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAA 1000

RESULT 7
US-10-479-674-90
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAA 1000

RESULT 8
US-10-479-674-91
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAA 1000

RESULT 9
US-10-121-120-169
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 28; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
Db 973 CAACTAACTATTGATGCTAAAGTTCAA 1000

RESULT 10
US-10-724-972A-3141
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match      100.0%; Score 28; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CAACTAACTATTGATGCTTAAGTTCAA 28
|||||
Db 994 CAACTAACTATTGATGCTTAAGTTCAA 1021

RESULT 11

US-10-398-221-10/c
; Sequence 10, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1163020
; TYPE: DNA
; ORGANISM: Listeria innocua
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u

US-10-398-221-10
Query Match 79.3%; Score 22.2; DB 8; Length 1163020;
Best Local Similarity 88.9%; Pred. No. 4.1e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTTAAGTTCAA 28
|||||
Db 391866 AACTAACTATTGATGCTTAAGTTCAA 391840

RESULT 12

US-10-398-221-2058/c
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua

US-10-398-221-2058
Query Match 79.3%; Score 22.2; DB 8; Length 3011208;
Best Local Similarity 88.9%; Pred. No. 4.7e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTTAAGTTCAA 28
|||||
Db 482132 AACTAACTATTGATGCTTAAGTTCAA 482106

RESULT 13

US-10-472-928-4935
; Sequence 4935, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: THE INSTITUTE FOR GENOMIC RESEARCH
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 4935
; LENGTH: 252
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-472-928-4935

Query Match 73.6%; Score 20.6; DB 9; Length 252;
Best Local Similarity 85.2%; Pred. No. 3.8e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AACTAACTATTGATGCTTAAGTTCAA 28
|||||
Db 5 AACTAACTATTGATGCTTAAGTTCAA 31

RESULT 14

US-10-617-320-379
; Sequence 379, Application US/10617320
; Publication No. US20050136404A1
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS

NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/617,320
FILING DATE: 10-Jul-2003

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998

APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 379:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid

FOR DIAG

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; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...270
; SEQUENCE DESCRIPTION: SEQ ID NO: 379:
US-10-617-320-379

Query Match      73.6%; Score 20.6; DB 10; Length 270;
Best Local Similarity 85.2%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 AACTAACTATTGATGCTAAAGTTCAAA 28
Db      62 AACTAACTTATGATGATAAAGTTTCAGA 88

RESULT 15
US-10-472-928-625
; Sequence 625, Application US/10472928
; Publication No. US20050020813A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026926WO
; CURRENT APPLICATION NUMBER: US/10/472,928
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: GB-0107658.7
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4979
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 625
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-472-928-625

Query Match      73.6%; Score 20.6; DB 9; Length 507;
Best Local Similarity 85.2%; Pred. No. 4.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 AACTAACTATTGATGCTAAAGTTCAAA 28
Db      5 AACTAACTTATGATGATAAAGTTTCAGA 31

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Search completed: May 31, 2006, 23:02:24
Job time : 733.424 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 10.716 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-25
Perfect score: 28
Sequence: 1 caactaactattgctgctaaagtctcaaa 28

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters: 493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	67.9	975	7	US-11-217-529-6080
2	18.4	65.7	594	7	US-11-217-529-166583
3	18	64.3	1087	6	US-10-953-349-6329
4	18	64.3	2020	7	US-11-293-697-1218
5	17.4	62.1	1359	6	US-10-953-349-15694
6	17.2	61.4	661	6	US-10-488-619-2732
7	17.2	61.4	1916	6	US-10-953-349-36474
8	17	60.7	541	6	US-10-488-619-949
9	17	60.7	1650	6	US-10-953-349-6680
10	17	60.7	2832	7	US-11-217-529-5260
11	17	60.7	3309	7	US-11-217-529-78086
12	16.8	60.0	606	7	US-11-217-529-79099
13	16.8	60.0	1004	6	US-10-953-349-17520
14	16.8	60.0	1584	6	US-10-953-349-4786
15	16.8	60.0	1608	6	US-10-953-349-13583
16	16.8	60.0	1908	7	US-11-217-529-80973
17	16.8	60.0	2016	7	US-11-217-529-2923
18	16.8	60.0	3495	7	US-11-293-697-463
19	16.8	60.0	3801	7	US-11-217-529-4511
20	16.8	60.0	3860	7	US-11-266-446-67
21	16.8	60.0	151830	6	US-10-519-335-37
22	16.6	59.3	1281	6	US-10-953-349-19184
23	16.6	59.3	2057	7	US-11-217-529-1780
24	16.6	59.3	2157	7	US-11-217-529-173838
25	16.4	58.6	435	6	US-10-488-619-270

C	26	16.4	58.6	648	7	US-11-217-529-842	Sequence 842, App
	27	16.4	58.6	771	7	US-11-217-529-5368	Sequence 5368, App
	28	16.4	58.6	1116	7	US-11-253-300-2	Sequence 2, Appli
	29	16.4	58.6	1292	6	US-10-953-349-27804	Sequence 27804, A
	30	16.4	58.6	1440	7	US-11-217-529-78387	Sequence 78387, A
C	31	16.4	58.6	1869	7	US-11-217-529-81293	Sequence 81293, A
	32	16.4	58.6	1965	7	US-11-217-529-4505	Sequence 4505, App
	33	16.4	58.6	2952	6	US-10-511-937-654	Sequence 654, App
C	34	16.2	57.9	1159	7	US-11-136-524-25	Sequence 25, Appl
	35	16.2	57.9	1173	7	US-11-217-529-312	Sequence 312, App
	36	16.2	57.9	1189	6	US-10-511-937-661	Sequence 661, App
	37	16.2	57.9	1695	7	US-11-217-529-81770	Sequence 81770, A
	38	16	57.1	622	7	US-11-217-529-191090	Sequence 191090,
C	39	16	57.1	924	7	US-11-217-529-365	Sequence 365, App
	40	16	57.1	1041	7	US-11-217-529-167027	Sequence 167027, A
C	41	16	57.1	1461	6	US-10-953-349-23227	Sequence 23227, A
	42	16	57.1	1476	7	US-11-217-529-4815	Sequence 4815, App
	43	16	57.1	2004	7	US-11-217-529-2004	Sequence 2004, App
	44	16	57.1	2691	7	US-11-217-529-460	Sequence 460, App
	45	16	57.1	3201	7	US-11-217-529-76871	Sequence 76871, A

ALIGNMENTS

RESULT 1
US-11-217-529-6080
; Sequence 6080, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAWA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6080
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-6080

Query Match 67.9%; Score 19; DB 7; Length 975;
Best Local Similarity 81.5%; Pred. No. 4.8;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CACTAATCTTTCATGCTTAAGTTCAA 27
DB 309 CTACTATCTATTGAACCTAAATTTCAA 335

RESULT 2
US-11-217-529-166583
; Sequence 166583, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAWA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166583
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166583

Query Match 65.7%; Score 18.4; DB 7; Length 594;
Best Local Similarity 78.6%; Pred. No. 8.3;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 CAACTAATTGATGCTAAAGTTCAA 28
Db 313 CAAGAAATCTTGGATGCTAAAGTTCAA 340

RESULT 3
US-10-953-349-6329
; Sequence 6329, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6329
; LENGTH: 1087
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6329

Query Match 64.3%; Score 18; DB 6; Length 1087;
Best Local Similarity 80.8%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACTAATATTGATGCTAAAGTTCAA 28
Db 910 ACTAATGATGATCTTATATTTCAGA 935

RESULT 4
US-11-293-697-1218
; Sequence 1218, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1218
; LENGTH: 2020
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1218

Query Match 64.3%; Score 18; DB 7; Length 2020;
Best Local Similarity 80.8%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 3 ACTAATATTGATGCTAAAGTTCAA 28

Db 1849 ACTAATATAGATGCAAAAGTCAAA 1874
RESULT 5
US-10-953-349-15694/c
; Sequence 15694, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15694
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-15694

Query Match 62.1%; Score 17.4; DB 6; Length 1359;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 AACTAATATTGATGCTAAAGTTCAA 28
Db 854 AACAAACGCTTGAAGCAAAAGTTGAAA 828

RESULT 6
US-10-488-619-2732
; Sequence 2732, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations, and Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2732
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2732

Query Match 61.4%; Score 17.2; DB 6; Length 661;
Best Local Similarity 86.4%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 7 ACTATTGATGCTAAAGTTCAA 28
Db 76 ACTAATGATGCTGAAGTTCCAA 97

RESULT 7
US-10-953-349-36474/c
; Sequence 36474, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3

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; SEQ ID NO 36474
; LENGTH: 1916
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1883)..(1883)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-36474

Query Match      61.4%; Score 17.2; DB 6; Length 1916;
Best Local Similarity 86.4%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAACTAACTATTGATGCTAAAG 22
    ||||| ||||| ||||| |||||
Db 1728 CAACTACTATTGAGGCTAAAG 1707

RESULT 8
US-10-488-619-949
; Sequence 949, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 99-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; PRIOR FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 949
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-949

Query Match      60.7%; Score 17; DB 6; Length 541;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTAACTATTGATGCTAAAGTTCAA 27
    ||||| ||||| ||||| |||||
Db 35 ACTAAATATTCAATGTTAAATTTCAA 59

RESULT 9
US-10-953-349-6680
; Sequence 6680, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 6680
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6680

Query Match      60.7%; Score 17; DB 6; Length 1650;
Best Local Similarity 80.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTAACTATTGATGCTAAAGTTCAA 27
    ||||| ||||| ||||| |||||
Db 561 ACTTACAATTGCTTCTAAAGGTTCAA 585
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RESULT 10
US-11-217-529-5260
; Sequence 5260, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5260
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5260

Query Match      60.7%; Score 17; DB 7; Length 2832;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 ACTAACTATTGATGCTAAAGTTCAA 27
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Db 798 ACCAACTACTACGCTAAAGTTCAA 822
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RESULT 11
US-11-217-529-78086
; Sequence 78086, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 78086
; LENGTH: 3309
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78086

Query Match      60.7%; Score 17; DB 7; Length 3309;
Best Local Similarity 80.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AACTAACTATTGATGCTAAAGTTCA 26
    ||||| ||||| ||||| |||||
Db 1634 AAATAACTTTGAATTCTAAAGTTCA 1658

RESULT 12
US-11-217-529-79099
; Sequence 79099, Application US/11217529
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; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79099
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79099

Query Match      60.0%; Score 16.8; DB 7; Length 606;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
||| ||| ||| ||| ||| ||| ||| |||
Db 322 CAAGAAATCTTTGACGCTAACGTTCAA 349

RESULT 13
US-10-953-349-17520
; Sequence 17520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17520
; LENGTH: 1004
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17520

Query Match      60.0%; Score 16.8; DB 6; Length 1004;
Best Local Similarity 90.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 8 CTATTGATGCTAAAGTTCAA 27
||| ||| ||| ||| ||| ||| |||
Db 398 CTTTGATCTCTAAAGTTCAA 417

RESULT 14
US-10-953-349-4786
; Sequence 4786, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4786
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; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-4786

Query Match      60.0%; Score 16.8; DB 6; Length 1584;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
||| ||| ||| ||| ||| ||| ||| |||
Db 344 CAACTTCTCTCGAAGCTATAGTTCACA 371

RESULT 15
US-10-953-349-13583
; Sequence 13583, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE:
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13583
; LENGTH: 1608
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-13583

Query Match      60.0%; Score 16.8; DB 6; Length 1608;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CAACTAACTATTGATGCTAAAGTTCAA 28
||| ||| ||| ||| ||| ||| ||| |||
Db 1204 CATCTACCAATTTGGTGTGAATTTGAAA 1231

Search completed: May 31, 2006, 21:22:04
Job time : 10.716 secs
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 87.1481 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-26
Perfect score: 39
Sequence: 1 cccaatttgatccattgttggtgatattatgtcttcaga 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
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- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	39	100.0	2007	2	US-08-743-637B-169 Sequence 169, App
C 2	39	100.0	2007	3	US-08-526-840B-169 Sequence 169, App
C 3	28	71.8	2028	3	US-09-134-001C-1710 Sequence 1710, App
C 4	23.2	59.5	11652	3	US-09-949-016-13413 Sequence 13413, A
5	22.6	57.9	2363	3	US-10-104-047-203 Sequence 203, App
6	22.4	57.4	4853	3	US-08-881-450A-22 Sequence 1244, App
7	22	56.4	563	3	US-09-621-976-1244 Sequence 1244, App
C 8	22	56.4	601	3	US-09-949-016-18896 Sequence 18896, A
C 9	22	56.4	601	3	US-09-949-016-56872 Sequence 56872, A
C 10	22	56.4	63591	3	US-09-949-016-11808 Sequence 11808, A
C 11	22	56.4	63591	3	US-09-949-016-13388 Sequence 13388, A
C 12	21.8	55.9	1451	3	US-09-465-558-37 Sequence 37, App
C 13	21.6	55.4	601	3	US-09-949-016-135878 Sequence 135878, A
C 14	21.6	55.4	601	3	US-09-949-016-135995 Sequence 135995, A
C 15	21.6	55.4	601	3	US-09-949-016-136112 Sequence 136112, A
16	21.6	55.4	193555	3	US-09-949-016-15553 Sequence 15553, A
17	21.6	55.4	193555	3	US-09-949-016-15554 Sequence 15554, A
18	21.6	55.4	193555	3	US-09-949-016-15555 Sequence 15555, A
19	21.4	54.9	126153	3	US-09-949-002-596 Sequence 596, App
20	21.4	54.9	135687	3	US-09-949-002-805 Sequence 805, App
21	21.4	54.9	818128	3	US-09-949-016-14546 Sequence 14546, A
22	21.4	54.9	818128	3	US-09-949-016-14547 Sequence 14547, A
23	21.4	54.9	818128	3	US-09-949-016-14548 Sequence 14548, A

24 21.4 54.9 818128 3 US-09-949-016-14549 Sequence 14549, A
25 21.4 54.9 818128 3 US-09-949-016-14550 Sequence 14550, A
26 21.4 54.9 818128 3 US-09-949-016-14551 Sequence 14551, A
27 21.4 54.9 818128 3 US-09-949-016-14552 Sequence 14552, A
28 21.4 54.9 818128 3 US-09-949-016-14553 Sequence 14553, A
29 21.4 54.9 818128 3 US-09-949-016-14554 Sequence 14554, A
30 21.4 54.9 818128 3 US-09-949-016-14555 Sequence 14555, A
31 21.4 54.9 818128 3 US-09-949-016-14556 Sequence 14556, A
32 21.4 54.9 818128 3 US-09-949-016-14557 Sequence 14557, A
33 21.4 54.9 818128 3 US-09-949-016-14558 Sequence 14558, A
34 21.4 54.9 818128 3 US-09-949-016-14559 Sequence 14559, A
35 21.4 54.9 818128 3 US-09-949-016-14560 Sequence 14560, A
36 21.4 54.9 818128 3 US-09-949-016-14561 Sequence 14561, A
37 21.4 54.9 818128 3 US-09-949-016-14562 Sequence 14562, A
38 21.4 54.9 818128 3 US-09-949-016-14564 Sequence 14564, A
39 21.4 54.9 818128 3 US-09-949-016-14565 Sequence 14565, A
40 21.4 54.9 818128 3 US-09-949-016-14566 Sequence 14566, A
41 21.4 54.9 818128 3 US-09-949-016-14567 Sequence 14567, A
C 42 21.2 54.4 729 3 US-09-248-796A-715 Sequence 715, App
43 21.2 54.4 740 3 US-09-721-341-10 Sequence 10, App
44 21.2 54.4 740 3 US-09-721-495B-10 Sequence 10, App
45 21.2 54.4 740 4 US-09-721-341-10 Sequence 10, App

ALIGNMENTS

RESULT 1

US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994066
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/526,840
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match      100.0%; Score 39; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
    |||||
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 2
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5000
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match      100.0%; Score 39; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
    |||||
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 3
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370

```

```

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      71.8%; Score 28; DB 3; Length 2028;
Best Local Similarity 97.5%; Pred. No. 0.58;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTGTTG-TTGATATAGTCTTCAGA 39
    |||||
Db 637 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 598

RESULT 4
US-09-949-016-13413/c
; Sequence 13413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13413
; LENGTH: 116652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(116652)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13413

Query Match      59.5%; Score 23.2; DB 3; Length 116652;
Best Local Similarity 77.8%; Pred. No. 57;
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CAATTTTGATCCATTGTTGTTGATATAGTCTTCAG 38
    |||||
Db 94872 CAATCTTGCTACATTGTTGTTGATATAGTCTTCAG 94837

RESULT 5
US-10-104-047-203
; Sequence 203, Application US/10104047
; Patent No. 6943241

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GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241el full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 203
LENGTH: 2363
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-203

Query Match 57.9%; Score 22.6; DB 3; Length 2363;
Best Local Similarity 75.7%; Pred. No. 54;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAG 38
|||||
DB 1896 CTAATTTAGATTCATTGTTGTTGATATAGTCTTCAG 1932
|||||

RESULT 6
US-08-881-450A-22
Sequence 22, Application US/08881450A
Patent No. 6274310
GENERAL INFORMATION:
APPLICANT: Habener, J.F. and Stoffers, D.A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: PANCREATIC DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Inc.
STREET: One Financial Center
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,450A
FILING DATE: June 24, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kathleen M. Williams
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 11275/7823
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4853 nucleotides
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: IPF1 gene, contig 1.

Query Match 57.4%; Score 22.4; DB 3; Length 4853;
Best Local Similarity 67.6%; Pred. No. 71;

Matches 23; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 5 ATTTTCATCCATTGTTGTTGATATAGTCTTCAG 38
|||||
DB 4507 ATTTGCATACATTTATTTWKAWATTTCTCCAG 4540
|||||

RESULT 7
US-09-621-976-1244
Sequence 1244, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 1244
LENGTH: 563
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 309..563
US-09-621-976-1244

Query Match 56.4%; Score 22; DB 3; Length 563;
Best Local Similarity 73.7%; Pred. No. 73;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAGA 39
|||||
DB 289 CTAAAGTCATCCATTCGTTATGATTTAGTCTTAAAGA 326
|||||

RESULT 8
US-09-949-016-18896/c
Sequence 18896, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18896
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-18896

Query Match 56.4%; Score 22; DB 3; Length 601;
Best Local Similarity 73.7%; Pred. No. 73;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTTCATCCATTGTTGTTGATATAGTCTTCAGA 39
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DB 581 CAAATTTTAATGCAITTCAGTTGATATCATCTTTTCATA 544
|||||

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RESULT 9
US-09-949-016-56872/c
; Sequence 56872, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56872
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636591)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-56872

Query Match          56.4%; Score 22; DB 3; Length 601;
Best Local Similarity 73.7%; Pred. No. 73;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTGATCCATTGTTGTGATATAGTCTTCAGA 39
| | | | | | | | | | | | | | | | | | | |
Db 581 CAAATTTTAATGCAATTCAGTTGATATCATTTTCATA 544

RESULT 10
US-09-949-016-11808/c
; Sequence 11808, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11808
; LENGTH: 636591
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636591)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11808

Query Match          56.4%; Score 22; DB 3; Length 636591;
Best Local Similarity 73.7%; Pred. No. 1.9e+02;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTGATCCATTGTTGTGATATAGTCTTCAGA 39
| | | | | | | | | | | | | | | | | | | |
Db 559594 CAAATTTTAATGCAATTCAGTTGATATCATTTTCATA 559557

RESULT 11
US-09-949-016-11808
; Sequence 11808, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11808
; LENGTH: 636591
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636591)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11808

Query Match          56.4%; Score 22; DB 3; Length 636591;
Best Local Similarity 73.7%; Pred. No. 1.9e+02;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2 CCAATTTGATCCATTGTTGTGATATAGTCTTCAGA 39
| | | | | | | | | | | | | | | | | | | |
Db 559594 CAAATTTTAATGCAATTCAGTTGATATCATTTTCATA 559557

RESULT 12
US-09-465-558-37/c
; Sequence 37, Application US/09465558
; Patent No. 6436657
; GENERAL INFORMATION:
; APPLICANT: Morakinyo, Layo O.
; TITLE OF INVENTION: TETRAHYDROFOLATE METABOLIC ENZYMES
; FILE REFERENCE: BB1322 US NA
; CURRENT APPLICATION NUMBER: US/09/465,558
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: 60/112,734
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 37
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Glycine max
US-09-465-558-37

Query Match          55.9%; Score 21.8; DB 3; Length 1451;
Best Local Similarity 78.8%; Pred. No. 98;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 CAAATTTGATCCATTGTTGTGATATAGTCTT 35
| | | | | | | | | | | | | | | | | | | |
Db 1409 CAAATTTTAATCCTTTTGTCTTGACTTAATCTT 1377

RESULT 13
US-09-949-016-135878/c
; Sequence 135878, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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Search completed: May 31, 2006, 21:13:16
Job time : 96.1481 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 1013.2 Seconds
(without alignments)
472.976 Million cell updates/sec

Title: US-09-865-579A-26

Perfect score: 39

Sequence: 1 cccaatttgatccattgtgtgatattcagtcagcaga 39

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- 3: /EMC Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
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- 9: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 14: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 15: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
- 16: /EMC Celerra_SIDS3/ptodata/2/pubpna/US10K_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	39	100.0	39	3	US-09-865-579A-26
3	39	100.0	560	10	US-10-478-633A-150
4	39	100.0	2007	3	US-09-452-599-169
5	39	100.0	2007	7	US-10-121-120-169
6	39	100.0	2007	9	US-10-479-674-78
7	39	100.0	2007	9	US-10-121-120-169
8	28	71.8	1957	9	US-10-479-674-82
9	28	71.8	2007	9	US-10-479-674-90
10	28	71.8	2028	8	US-10-724-972A-3141
11	26.4	67.7	2007	9	US-10-479-674-91
12	23.2	59.5	287	9	US-10-425-115-7606
13	23.2	59.5	777	4	US-09-925-065A-938424
14	23.2	59.5	777	4	US-09-925-065A-938424
15	23	59.0	3009	13	US-11-097-143-37397
16	23	59.0	5293	13	US-11-097-143-37396
17	23	59.0	25988	13	US-11-097-143-11350

Sequence 1285, Ap	1511	58.5	22.8	18	9	US-10-363-345A-1285
Sequence 1286, Ap	1511	58.5	22.8	19	9	US-10-363-345A-1286
Sequence 1285, Ap	1511	58.5	22.8	20	10	US-10-363-483A-1285
Sequence 1286, Ap	1511	58.5	22.8	21	10	US-10-363-483A-1286
Sequence 13277, A	1641	58.5	22.8	22	8	US-10-424-599-13277
Sequence 78841, A	5424	58.5	22.8	23	8	US-10-437-963-78841
Sequence 91, Appl	426	57.9	22.6	24	3	US-09-813-358-91
Sequence 91, Appl	426	57.9	22.6	25	3	US-09-997-279-91
Sequence 574125, A	559	57.9	22.6	26	4	US-09-925-065A-574125
Sequence 574126, A	559	57.9	22.6	27	4	US-09-925-065A-574126
Sequence 574127, A	559	57.9	22.6	28	4	US-09-925-065A-574127
Sequence 574125, A	559	57.9	22.6	29	5	US-09-925-065A-574125
Sequence 574126, A	559	57.9	22.6	30	5	US-09-925-065A-574126
Sequence 574127, A	559	57.9	22.6	31	5	US-09-925-065A-574127
Sequence 45481, A	600	57.9	22.6	32	10	US-10-972-079-45481
Sequence 65295, A	647	57.9	22.6	33	9	US-10-425-115-65295
Sequence 27147, A	894	57.9	22.6	34	9	US-10-424-599-27147
Sequence 565340, A	995	57.9	22.6	35	12	US-10-301-480-565340
Sequence 1178749, A	995	57.9	22.6	36	12	US-10-301-480-1178749
Sequence 80249, A	1707	57.9	22.6	37	8	US-10-437-963-80249
Sequence 55, Appl	1921	57.9	22.6	38	10	US-10-487-092-55
Sequence 23786, A	2212	57.9	22.6	39	8	US-10-437-963-23786
Sequence 203, Appl	2363	57.9	22.6	40	7	US-10-104-047-203
Sequence 203, Appl	2363	57.9	22.6	41	16	US-11-072-512-203
Sequence 81142, A	2490	57.9	22.6	42	8	US-10-437-963-81142
Sequence 96408, A	2685	57.9	22.6	43	8	US-10-437-963-96408
Sequence 29787, A	2742	57.9	22.6	44	8	US-10-437-963-29787
Sequence 29785, A	3018	57.9	22.6	45	8	US-10-437-963-29785

ALIGNMENTS

RESULT 1

US-09-865-579A-8
; Sequence 8, Application US/09865579A
; Patent No. US2002009492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; CURRENT APPLICATION NUMBER: US/09/865,579A
; FILE REFERENCE: 9558-003-27
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide capable of binding specifically to mecA gene
; OTHER INFORMATION: or RNA derived from said gene

US-09-865-579A-8
Query Match 100.0%; Score 39; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 1 CCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39

RESULT 2

US-09-865-579A-26
; Sequence 26, Application US/09865579A

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; Patent No. US20020098492A1
; GENERAL INFORMATION:
; APPLICANT: Taya, Toshiaki
; APPLICANT: Ishiguro, Takahiko
; APPLICANT: Saito, Juichi
; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of
; TITLE OF INVENTION: Methicillin Resistant Staphylococcus Aureus
; FILE REFERENCE: 9558-003-27
; CURRENT APPLICATION NUMBER: US/09/865,579A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: JP 2000-163149
; PRIOR FILING DATE: 2000-05-29
; PRIOR APPLICATION NUMBER: JP 2000-179394
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 26
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-865-579A-26

Query Match          100.0%; Score 39; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39

RESULT 3
US-10-478-633A-150/c
; Sequence 150, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
; TITLE OF INVENTION: acid amplification or detection reaction
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 150
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-478-633A-150

Query Match          100.0%; Score 39; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 375 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 337

RESULT 4
US-09-452-599-169/c
; Sequence 169, Application US/09452599
; Patent No. US20020055101A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers

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; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/09/452,599
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/526,840
; PRIOR FILING DATE: 1995-09-11
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-452-599-169

Query Match          100.0%; Score 39; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 5
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20030180733A1
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match          100.0%; Score 39; DB 7; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 6
US-10-479-674-78/c
; Sequence 78, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS

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; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-78

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 7
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-121-120-169

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 615 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 8
US-10-479-674-82/c
; Sequence 82, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTAN
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
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; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-82

Query Match      71.8%; Score 28; DB 9; Length 1957;
Best Local Similarity 97.5%; Pred. No. 13;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 566 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 527

RESULT 9
US-10-479-674-90/c
; Sequence 90, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Rosebach, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTAN
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match      71.8%; Score 28; DB 9; Length 2007;
Best Local Similarity 97.5%; Pred. No. 13;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 39
Db 616 CCCAATTTTGATCCATTGTTGTTGATATAGTCTTCAGA 577

RESULT 10
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
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US-10-724-972A-3141

Query Match 71.8%; Score 28; DB 8; Length 2028;
Best Local Similarity 97.5%; Pred. No. 13;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCCAATTTGTTG-TTGATATAGTCTTCAGA 39
Db 637 CCCAATTTTGATCCCAATTTGTTGTTGATATAGTCTTCAGA 598

RESULT 11

US-10-479-674-91/c

; Sequence 91, Application US/10479674

; Publication No. US2005001993A1

; GENERAL INFORMATION:

; APPLICANT: Infectio Diagnostica (I.D.I.) Inc.

; APPLICANT: Huletsky, Ann

; APPLICANT: Roszbach, Valery

; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT

; FILE REFERENCE: TV/12287.92

; CURRENT APPLICATION NUMBER: US/10/479,674

; CURRENT FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: CA 2,348,042

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 91

; LENGTH: 2007

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-10-479-674-91

Query Match

Best Local Similarity 67.7%; Score 26.4; DB 9; Length 2007;

Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CCCAATTTTGATCCCAATTTGTTG-TTGATATAGTCTTCAGA 39
Db 616 CCCAATTTTGATCCCAATTTGTTGTTGATATAGTCTTCAGA 577

RESULT 12

US-10-425-115-7606

; Sequence 7606, Application US/10425115

; Publication No. US2004021427A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(S3222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 7606

; LENGTH: 287

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)-(287)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: M74577_106935C.1

US-10-425-115-7606

Query Match

Best Local Similarity 59.5%; Score 23.2; DB 9; Length 287;

Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 AATTTTGATCCCAATTTGTTGTTGATATAGTCTTCAGA 39
Db 125 AAGATTGATCCAGTAGGTGTTGATTATTCTTCAAA 160

RESULT 13

US-09-925-065A-938424/c

; Sequence 938424, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 938424

; LENGTH: 777

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-938424

Query Match

Best Local Similarity 59.5%; Score 23.2; DB 4; Length 777;

Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CAATTTTGATCCCAATTTGTTGTTGATATAGTCTTCAG 38
Db 465 CAATCTTGCTACATTTGTTTATAGATATAATGTCAG 430

RESULT 14

US-09-925-065A-938424/c

; Sequence 938424, Application US/09925065A

; Publication No. US20050228172A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 938424

; LENGTH: 777

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-938424

Query Match

Best Local Similarity 59.5%; Score 23.2; DB 5; Length 777;

Best Local Similarity 77.8%; Pred. No. 5e+02; Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 CAAATTTTGATCCATTTGTTGTTGATATAGTCTTCAG 38
|||||
Db 465 CAAATCTTGCTACATTTGTTTGTAGATATAATGTCAG 430

RESULT 15

US-11-097-143-37397/c
; Sequence 37397, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37397
; LENGTH: 3009
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-37397

Query Match 59.0%; Score 23; DB 13; Length 3009;
Best Local Similarity 74.4%; Pred. No. 8.1e+02; Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CCCAATTTTGATCCATTTGTTGTTGATATAGTCTTCAGA 39
|||||
Db 2625 CGCAATTTTGAGCACTTCGTTTTTGTATAGTCGTCAAA 2587

Search completed: May 31, 2006, 23:02:25
Job time : 1013.2 secs

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:19:51 ; Search time 14.9259 Seconds
(without alignments)
307.732 Million cell updates/sec

Title: US-09-865-579A-26
Perfect score: 39
Sequence: 1 cccaatttgatccattgttgatagatagcttcaga 39

Scoring table: IDENTITY_NUC
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Searched: 246837 seqs, 5886990 residues

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Maximum Match 100%
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 - 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	56.4	1556	US-10-953-349-17882	Sequence 17882, A
2	20.8	53.3	1257	US-11-217-529-1620	Sequence 1620, Ap
3	20.6	52.8	1262	US-10-953-349-20828	Sequence 20828, A
C 4	20.4	52.3	678	US-11-217-529-3208	Sequence 3208, Ap
5	20.2	51.8	1361	US-10-953-349-3924	Sequence 3924, Ap
C 6	20	51.3	3075	US-11-217-529-77428	Sequence 77428, A
C 7	19.8	50.8	1000	US-11-233-726-20	Sequence 20, Appl
C 8	19.8	50.8	2089	US-10-953-349-22930	Sequence 22930, A
C 9	19.8	50.8	2772	US-11-217-529-75755	Sequence 75755, A
C 10	19.8	50.8	3230	US-11-293-697-2392	Sequence 2392, Ap
11	19.6	50.3	1794	US-11-217-529-81556	Sequence 81556, A
12	19.6	50.3	1871	US-10-953-349-6075	Sequence 6075, Ap
C 13	19.4	49.7	810	US-11-217-529-82386	Sequence 82386, A
C 14	19.4	49.7	1110	US-11-217-529-1784	Sequence 1784, Ap
C 15	19.4	49.7	2130	US-11-217-529-80690	Sequence 80690, A
C 16	19.4	49.7	2631	US-10-527-411-65	Sequence 65, Appl
C 17	19.4	49.7	2727	US-10-527-411-63	Sequence 63, Appl
C 18	19.4	49.7	2745	US-10-527-411-59	Sequence 59, Appl
C 19	19.4	49.7	2850	US-10-527-411-67	Sequence 67, Appl
C 20	19.4	49.7	3393	US-10-527-411-138	Sequence 138, Appl
C 21	19.4	49.7	4127	US-11-251-610-10	Sequence 10, Appl
C 22	19.2	49.2	498	US-10-953-349-6839	Sequence 6839, Ap
C 23	19.2	49.2	1698	US-11-217-529-482	Sequence 482, Appl
C 24	19.2	49.2	1759	US-10-504-120-1	Sequence 1, Appl
25	19.2	49.2	3132	US-11-217-529-77436	Sequence 77436, A

C 26	19.2	49.2	3396	7	US-11-217-529-75365	Sequence 75365, A
C 27	19	48.7	1290	7	US-11-302-678-54	Sequence 54, Appl
C 28	19	48.7	1413	7	US-11-217-529-173427	Sequence 173427, A
C 29	19	48.7	1557	7	US-11-302-678-52	Sequence 52, Appl
C 30	19	48.7	2346	7	US-11-251-610-18	Sequence 18, Appl
C 31	19	48.7	2361	7	US-11-293-697-493	Sequence 493, Appl
C 32	19	48.7	3247	7	US-11-251-610-3	Sequence 3, Appl
C 33	19	48.7	3336	7	US-11-217-529-80440	Sequence 80440, A
C 34	19	48.7	4852	6	US-10-505-928-417	Sequence 417, Appl
C 35	19	48.7	394191	6	US-10-506-549-3	Sequence 3, Appl
C 36	18.8	48.2	1336	6	US-10-953-349-24839	Sequence 24839, A
C 37	18.8	48.2	1548	7	US-11-217-529-6018	Sequence 6018, Ap
C 38	18.8	48.2	1656	7	US-11-217-529-79362	Sequence 79362, A
C 39	18.8	48.2	1662	6	US-10-953-349-16829	Sequence 16829, A
C 40	18.8	48.2	2476	6	US-10-501-834-211	Sequence 211, Appl
C 41	18.6	47.7	51	7	US-11-245-248-363	Sequence 363, Appl
C 42	18.6	47.7	276	7	US-11-263-326-115	Sequence 115, Appl
C 43	18.6	47.7	321	7	US-11-217-529-77583	Sequence 77583, A
C 44	18.6	47.7	660	7	US-11-217-529-1813	Sequence 1813, Ap
C 45	18.6	47.7	1011	7	US-11-217-529-173708	Sequence 173708, A

ALIGNMENTS

RESULT 1

US-10-953-349-17882
; Sequence 17882, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17882
; LENGTH: 1556
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-17882

Query Match 56.4%; Score 22; DB 6; Length 1556;
Best Local Similarity 73.7%; Pred. No. 5.7;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy	2	CCAAATTTTCATCCATTGTTGTTGATATAGTCTTCACA	39
Db	274	CAAAATGTTGATCCAAATGATGTTGTTAGAAACATCACA	311

RESULT 2

US-11-217-529-1620
; Sequence 1620, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1620

; LENGTH: 1257
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1620

Query Match 53.3%; Score 20.8; DB 7; Length 1257;
Best Local Similarity 78.1%; Pred. No. 15;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TTTTGATCCATTGTTGTGATAGTCTTCAC 37
||| ||||||| ||| |||||||
DB 237 TTATGAAGCACTGTTGTTTATATACATCTTCA 268

RESULT 3
US-10-953-349-20828
; Sequence 20828, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20828
; LENGTH: 1262
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20828

Query Match 52.8%; Score 20.6; DB 6; Length 1262;
Best Local Similarity 74.3%; Pred. No. 18;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 CAATTTGATCCATTGTTGTGATAGTCTTCA 37
||| ||||||| ||| |||||||
DB 1090 CAACTATGATCCTTTGTTTAATATCTAGTCTTTA 1124

RESULT 4
US-11-217-529-3208/c
; Sequence 3208, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3208
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3208

Query Match 52.3%; Score 20.4; DB 7; Length 678;
Best Local Similarity 71.1%; Pred. No. 19;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 CCCAAATTTGATCCATTGTTGTGATAGTCTTCAG 38
||| ||||||| ||| |||||||

Db 595 CCACAATTTCTTCTGTTTGCCTGGACGTTGCTCTTGAG 558

RESULT 5
US-10-953-349-3924
; Sequence 3924, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3924
; LENGTH: 1361
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3924

Query Match 51.8%; Score 20.2; DB 6; Length 1361;
Best Local Similarity 75.8%; Pred. No. 26;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 6 TTTTGATCCATTGTTGTGATAGTCTTCCAG 38
||| ||||||| ||| |||||||
DB 1205 TTTTGTCATTTGCTTTGGATATGTTCTCTCG 1237

RESULT 6
US-11-217-529-77428/c
; Sequence 77428, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77428
; LENGTH: 3075
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77428

Query Match 51.3%; Score 20; DB 7; Length 3075;
Best Local Similarity 72.2%; Pred. No. 35;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 CCCAAATTTGATCCATTGTTGTGATAGTCTTCC 36
||| ||||||| ||| |||||||
DB 2784 CCAAATTTTATCATATTTCTTGTGTTATATCTCC 2749

RESULT 7
US-11-233-726-20/c
; Sequence 20, Application US/11233726
; Publication No. US20060090216A1
; GENERAL INFORMATION:
; APPLICANT: APUIA, Nestor
; APPLICANT: KWOK, Shing
; APPLICANT: ALEXANDROV, Nikolai

```

; APPLICANT: TATARINOVA, Tatiana
; APPLICANT: FANG, Yiwen
; APPLICANT: PENNELL, Roger
; APPLICANT: LU, Yu-Ping
; APPLICANT: MEDRANO, Leonard
; APPLICANT: FELDMANN, Kenneth A.
; APPLICANT: COOK, Zhihong C.
; TITLE OF INVENTION: Promoter, Promoter Control Elements, And Combinations, And Uses
; FILE REFERENCE: 2750-1619PUS2
; CURRENT APPLICATION NUMBER: US/11/233,726
; PRIOR FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/612,891
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/613,134
; PRIOR FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/637,174
; PRIOR FILING DATE: 2004-12-16
; NUMBER OF SEQ ID NOS: 46
; SEQ ID NO 20
; LENGTH: 1000
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1022)..(1022)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1000)
; OTHER INFORMATION: Ceres Promoter construct YP0337 as found in Promoter Report #143
US-11-233-726-20

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Query Match      50.8%; Score 19.8; DB 7; Length 1000;
Best Local Similarity 77.4%; Pred. No. 34;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      5  ATTTGATCCATTTGTTGTCATATAGTCCTT 35
      | ||||| | ||||| | |||||
Db      253 AATTGATATATATGTTGTTGTTTCGTCCTT 223

RESULT 8
US-10-953-349-22930/c
; Sequence 22930, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22930
; LENGTH: 2089
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22930

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```

Query Match      50.8%; Score 19.8; DB 6; Length 2089;
Best Local Similarity 69.2%; Pred. No. 39;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 CCCAAATTTTCATCCATTGTTGGTTGATATAGTCTTTCAGA 39
      |||||
Db 1840 CTCAAATTTTCACACCCCTTGTTGGTTGCTCTGGTTTTCATA 1802
      |||||

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RESULT 9
US-11-217-529-75755/c
; Sequence 75755, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75755
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75755
Query Match 50.8%; Score 19.8; DB 7; Length 2772;
Best Local Similarity 77.4%; Pred. No. 41;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 CAATTTTGATCCATTGTTGTTGATATAGTC 33
||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 CAAACGTGAACGATTGTTGTTGATTAAAGTC 121

RESULT 10
US-11-293-697-2392/c
; Sequence 2392, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2392
; LENGTH: 3230
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-2392
Query Match 50.8%; Score 19.8; DB 7; Length 3230;
Best Local Similarity 69.2%; Pred. No. 42;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CCCAAATTGATCCATTGTTGTTGATATAGTCATGCTTCAGA 39
||||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2212 CCCAACTTAGATCTATTTGCTCTCTTATGGACCTGTGA 2174

RESULT 11
US-11-217-529-81556
; Sequence 81556, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO

```

```
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81556
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1767)..(1768)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-81556

Query Match      50.3%; Score 19.6; DB 7; Length 1794;
Best Local Similarity 84.6%; Pred. No. 44;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ATTTGATCCATTGTTGTTGATATA 30
Db 929 ATTTGATCCATTGATGTTAATA 954
|||||
|||||

RESULT 12
US-10-953-349-6075
; Sequence 6075, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6075
; LENGTH: 1871
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6075

Query Match      50.3%; Score 19.6; DB 6; Length 1871;
Best Local Similarity 73.5%; Pred. No. 45;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 4 AATTTTGATCCATTGTTGTTGATAGTCTTCA 37
Db 1760 AATTTGTTTATTGTTGTTTGAATAGTAGTTA 1793
|||||
|||||
|||||
|||||

RESULT 13
US-11-217-529-82386/c
; Sequence 82386, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82386
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82386

Query Match      49.7%; Score 19.4; DB 7; Length 810;
Best Local Similarity 70.3%; Pred. No. 45;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 CCAATTTTGATCCATTGTTGTTGATATAGTCTTCAG 38
Db 377 CCAATGATGATGATTTGTTGTCGGATTGTCATCAG 341
|||||
|||||
|||||
|||||

RESULT 14
US-11-217-529-1784/c
; Sequence 1784, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1784
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1784

Query Match      49.7%; Score 19.4; DB 7; Length 1110;
Best Local Similarity 70.3%; Pred. No. 48;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 CCAATTTTGATCCATTGTTGTTGATATAGTCTTCAG 38
Db 377 CCAATTTGTCATCCCGTTGTTGATATCTTTCAG 341
|||||
|||||
|||||
|||||

RESULT 15
US-11-217-529-80690/c
; Sequence 80690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80690
; LENGTH: 2130
; TYPE: DNA
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80690

Query Match	49.7%;	Score 19.4;	DB 7;	Length 2130;
Best Local Similarity	70.3%;	Pred. No. 54;		
Matches 26;	Conservative	0;	Mismatches 11;	Indels 0;
			Gaps 0;	

Qy 2 CCAATTTGATCATTTGTGGTATAGTCTTCAG 38
 ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db , 1592 CGGAATTCATCAATTTGTCCCTGATGCTCTTAG 1556

Search completed: May 31, 2006, 21:22:05
Job time : 14.9259 secs

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OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:03:44 ; Search time 87.1481 Seconds
(without alignments)
837.347 Million cell updates/sec

Title: US-09-865-579A-27

Perfect score: 39

Sequence: 1 tttttttttcttataatgatgtgcattgtattgc 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1 COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5 COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7 COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	89	3	US-09-109-329-4
2	39	100.0	108	3	US-09-109-329-13
3	39	100.0	2007	2	US-08-743-637B-169
4	39	100.0	2007	3	US-08-526-840B-169
5	39	100.0	2028	3	US-09-134-001C-1710
6	29	74.4	59	3	US-09-109-329-3
7	25.2	64.6	3034	3	US-09-799-451-517
8	24.2	62.1	914	3	US-09-227-357-123
9	24.2	62.1	914	3	US-09-973-278-36
10	24.2	62.1	6254	3	US-08-956-171E-404
11	24.2	62.1	6254	3	US-08-781-986A-404
12	24.2	62.1	9262	3	US-09-566-921-74
13	24.2	62.1	107937	3	US-09-949-016-17192
14	24	61.5	36	3	US-09-109-329-14
15	24	61.5	36	3	US-09-109-329-15
16	23.6	60.5	601	3	US-09-949-016-188971
17	23.6	60.5	26664	3	US-09-564-805-28
18	23.6	60.5	26664	3	US-09-434-382-28
19	23.6	60.5	29558	3	US-09-949-016-15607
20	23.6	60.5	83349	3	US-09-949-016-17149
21	23.6	60.5	256287	3	US-09-949-016-14608
22	23	59.0	590	4	US-09-880-107-98
23	23	59.0	1210	3	US-09-023-655-594

24	23	59.0	2082	3	US-09-149-476-257	Sequence 257, App
25	23	59.0	60110	3	US-09-949-016-17338	Sequence 17338, A
26	23	59.0	60110	3	US-09-949-016-17339	Sequence 17339, A
27	23	59.0	61083	3	US-09-949-016-14144	Sequence 14144, A
28	23	59.0	61083	3	US-09-949-016-14145	Sequence 14145, A
29	22.6	57.9	601	3	US-09-949-016-161878	Sequence 161878, A
30	22.6	57.9	1848	3	US-09-323-998B-46	Sequence 46, Appl
31	22.6	57.9	2428	3	US-09-731-166-5	Sequence 5, Appl
32	22.6	57.9	36618	3	US-09-949-016-15723	Sequence 15723, A
33	22.6	57.9	49011	3	US-09-949-016-14221	Sequence 14221, A
34	22.6	57.9	65990	3	US-09-949-016-11830	Sequence 11830, A
35	22.6	57.9	144362	3	US-09-949-016-16066	Sequence 16066, A
36	22.6	57.9	153866	3	US-09-949-016-16919	Sequence 16919, A
37	22.6	57.9	238815	3	US-09-949-016-16274	Sequence 16274, A
38	22.2	56.9	13866	3	US-09-949-016-17252	Sequence 17252, A
39	22.2	56.9	44789	3	US-09-949-016-13909	Sequence 13909, A
40	22	56.4	601	3	US-09-949-016-85526	Sequence 85526, A
41	22	56.4	601	3	US-09-949-016-85527	Sequence 85527, A
42	22	56.4	601	3	US-09-949-016-178468	Sequence 178468, A
43	22	56.4	953	3	US-09-270-767-6678	Sequence 6678, Ap
44	22	56.4	953	3	US-09-270-767-21960	Sequence 21960, A
45	22	56.4	99830	3	US-09-949-016-16859	Sequence 16859, A

ALIGNMENTS

RESULT 1

US-09-109-329-4
; Sequence 4, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 89
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-4

Query Match	100.0%	Score 39;	DB 3;	Length 89;
Best Local Similarity	100.0%	Pred No. 0.00026;		
Mismatches	39;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	TTTTCTTTCTCTATTAATGATGCGATTGTCG 39		
DB	43	TTTTCTTTCTCTATTAATGATGCGATTGTCG 81		

RESULT 2

US-09-109-329-13/c
; Sequence 13, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-13

Query Match 100.0%; Score 39; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGGATTGTATTGC 39
DB 49 TTTTCTTTTCTCTATTATGATGCGGATTGTATTGC 11

RESULT 3
US-08-743-637B-169/c
; Sequence 169, Application US/08743637B
; Patent No. 5994086
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: PICARD, Francois J.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 EAST WISCONSIN AVENUE
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,637B
; FILING DATE: 04-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE: 11-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-743-637B-169

Query Match 100.0%; Score 39; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGGATTGTATTGC 39
DB 955 TTTTCTTTTCTCTATTATGATGCGGATTGTATTGC 917

RESULT 4
US-08-526-840B-169/c
; Sequence 169, Application US/08526840B
; Patent No. 6001564
; GENERAL INFORMATION:
; APPLICANT: BERGERON, Michel G.
; APPLICANT: OUELLETTE, Marc
; APPLICANT: ROY, Paul H.
; TITLE OF INVENTION: SPECIFIC AND UNIVERSAL PROBES AND
; TITLE OF INVENTION: AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
; TITLE OF INVENTION: COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
; TITLE OF INVENTION: FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
; NUMBER OF SEQUENCES: 177
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/526,840B
; FILING DATE: 11-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/304,732
; FILING DATE: 12-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 850586.90012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5591
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2007 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-526-840B-169

Query Match 100.0%; Score 39; DB 3; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGGATTGTATTGC 39
DB 955 TTTTCTTTTCTCTATTATGATGCGGATTGTATTGC 917

RESULT 5
US-09-134-001C-1710/c
; Sequence 1710, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCU.
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13


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; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1710
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (52)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-134-001C-1710

Query Match      100.0%; Score 39; DB 3; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTATTAAATGATGCGGATGTTATGC 39
Db 976 TTTTCTTTTCTATTAAATGATGCGGATGTTATGC 938

RESULT 6
US-09-109-329-3/c
; Sequence 3, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: STAPHYLOCOCCI
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 59
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: meca Gene from Staphylococcal Species
US-09-109-329-3

Query Match      74.4%; Score 29; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTATTAAATGATGCGG 29
Db 29 TTTTCTTTTCTATTAAATGATGCGG 1

RESULT 7
US-09-799-451-517
; Sequence 517, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyang
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aigong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Junding
; APPLICANT: Yamazaki, Victoria
```

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; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 517
; LENGTH: 3034
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (729)..(917)
US-09-799-451-517

Query Match      64.6%; Score 25.2; DB 3; Length 3034;
Best Local Similarity 78.9%; Pred. No. 15;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTATTAAATGATGCGGATGTTATGC 38
Db 2585 TATTTTGTATATATATGCTGTCGATGTTATGC 2622

RESULT 8
US-09-227-357-123/c
; Sequence 123, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
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; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (909)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-227-357-123

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Query Match 62.1%; Score 24.2; DB 3; Length 914;
Best Local Similarity 78.4%; Pred. No. 29;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 1 TTTTCTTTTCTTATTATGTATGCGATTGTATT 37
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Db 872 TTTTCTTTTCTTATTATGTATGCGATTGTATT 836

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RESULT 9
US-09-973-278-36/c
; Sequence 36, Application US/09973278
; Patent No. 6924354
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P2
; CURRENT APPLICATION NUMBER: US/09/973,278
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 60/239,899
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/051,926

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; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: 1997-07-08
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; PRIOR FILING DATE: 1997-07-08
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; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: 60/055,722
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,723
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,948
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,949
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,953
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,950
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,947
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,964
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/056,360
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (909)---(909)
; OTHER INFORMATION: n equals a,t,g, or c

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US-09-973-278-36

Query Match 62.1%; Score 24.2; DB 3; Length 914;
Best Local Similarity 78.4%; Pred. No. 29;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGATTGTATT 37
|||||
Db 872 TTTTCTTTTCTCTATTATGATGCGATTGTATT 836

RESULT 10

US-08-956-171E-404/C
; Sequence 404, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 404:
SEQUENCE CHARACTERISTICS:
LENGTH: 6254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 404:

US-08-956-171E-404
Query Match 62.1%; Score 24.2; DB 3; Length 6254;
Best Local Similarity 78.4%; Pred. No. 35;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGATTGTATT 37
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Db 2565 TTTTCTTTTCTCTATTATGATGCGATTGTATT 2529

RESULT 11

US-08-781-986A-404/C
; Sequence 404, Application US/08781986A

; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 404:
SEQUENCE CHARACTERISTICS:
LENGTH: 6254 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-404

Query Match 62.1%; Score 24.2; DB 3; Length 6254;
Best Local Similarity 78.4%; Pred. No. 35;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTATGATGCGATTGTATT 37
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Db 2565 TTTTCTTTTCTCTATTATGATGCGATTGTATT 2529

RESULT 12

US-09-566-921-74
; Sequence 74, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debra W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 74
; LENGTH: 9262
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 246655.92
; NAME/KEY: unsure
; LOCATION: 1941-1942, 1952-1953, 1956, 1958, 1963, 6600-6601
; OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-74

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Query Match          62.1%; Score 24.2; DB 3; Length 9262;
Best Local Similarity 78.4%; Pred. No. 36;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAATGATGCGATTGTATT 37
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DB 2454 TTTTCTATTTCAGTATTAACTCTGTGGCTTGTATT 2490

RESULT 13
US-09-949-016-17192
; Sequence 17192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17192
; LENGTH: 107937
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(107937)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17192

Query Match          62.1%; Score 24.2; DB 3; Length 107937;
Best Local Similarity 78.4%; Pred. No. 46;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAATGATGCGATTGTATT 37
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 85597 TGTCTTCTCTCTCTTTTCATTTAATCTGGGATTGTGT 85633

RESULT 14
US-09-109-329-14/c
; Sequence 14, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-14

Query Match          61.5%; Score 24; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAATGATGAT 24
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DB 24 TTTTCTTTTCTCTATTAATGAT 1

RESULT 15
US-09-109-329-15/c
; Sequence 15, Application US/09109329
; Patent No. 6503709
; GENERAL INFORMATION:
; APPLICANT: Bekkaoui, Faouzi
; APPLICANT: Cloney, Lynn P.
; TITLE OF INVENTION: METHODS FOR RAPIDLY DETECTING METHICILLIN RESISTANT
; FILE REFERENCE: 480094.424
; CURRENT APPLICATION NUMBER: US/09/109,329
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Solid Phase
; OTHER INFORMATION: Synthesis of Nucleic Acid Probe Complementary to
; OTHER INFORMATION: mecA Gene from Staphylococcal Species
US-09-109-329-15

Query Match          61.5%; Score 24; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAATGAT 24
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 24 TTTTCTTTTCTCTATTAATGAT 1

Search completed: May 31, 2006, 21:13:18
Job time : 89.1481 secs
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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2006, 21:16:53 ; Search time 1013.2 Seconds

(without alignments)

472.976 Million cell updates/sec

Title: US-09-865-579A-27

Perfect score: 39

Sequence: 1 tttttttttcttataatgattggtgattgattgc 39

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	US-09-865-579A-27	Sequence 27, Appl
2	39	100.0	1957	US-10-479-674-82	Sequence 82, Appl
3	39	100.0	2007	US-09-452-599-169	Sequence 169, Appl
4	39	100.0	2007	US-10-121-120-169	Sequence 169, Appl
5	39	100.0	2007	US-10-479-674-78	Sequence 78, Appl
6	39	100.0	2007	US-10-479-674-90	Sequence 90, Appl
7	39	100.0	2007	US-10-479-674-91	Sequence 91, Appl
8	39	100.0	2007	US-10-121-120-169	Sequence 169, Appl
9	39	100.0	2028	US-10-724-972A-3141	Sequence 3141, Appl
10	25.2	64.6	3034	US-10-302-172-517	Sequence 517, Appl
11	24.6	63.1	644	US-09-925-065A-827806	Sequence 827806, Appl
12	24.6	63.1	644	US-09-925-065A-827807	Sequence 827807, Appl
13	24.6	63.1	644	US-09-925-065A-827806	Sequence 827806, Appl
14	24.6	63.1	644	US-09-925-065A-827807	Sequence 827807, Appl
15	24.2	62.1	343	US-10-674-124A-21698	Sequence 21698, A
16	24.2	62.1	685	US-10-027-632-109982	Sequence 109982, A
17	24.2	62.1	685	US-10-027-632-109982	Sequence 109982, A

ALIGNMENTS

RESULT 1

US-09-865-579A-27

; Sequence 27, Application US/09865579A

; Patent No. US2002009492A1

; GENERAL INFORMATION:

; APPLICANT: Taya, Toshiki

; APPLICANT: Saio, Juichi

; TITLE OF INVENTION: Oligonucleotides and Method for Detection of mecA Gene of

; FILE OF INVENTION: Methicillin Resistant Staphylococcus Aureus

; FILE REFERENCE: 9558-003-27

; CURRENT APPLICATION NUMBER: US/09/865,579A

; PRIOR FILING DATE: 2001-05-29

; PRIOR APPLICATION NUMBER: JP 2000-163149

; PRIOR FILING DATE: 2000-05-29

; PRIOR APPLICATION NUMBER: JP 2000-179394

; PRIOR FILING DATE: 2000-06-09

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 27

; LENGTH: 39

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Probe

US-09-865-579A-27

Query Match 100.0%; Score 39; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0053;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTTTCTTTTCTTCTTATGATGATGCGGATGTTATGCG 39

Db 1 TTTTCTTTTCTTCTTATGATGATGCGGATGTTATGCG 39

RESULT 2

US-10-479-674-82/C

; Sequence 82, Application US/10479674

; Publication No. US20050019893A1

Sequence 4505, Ap
Sequence 8471, Ap
Sequence 7879, Ap
Sequence 1828, Ap
Sequence 123, App
Sequence 123, App
Sequence 36, Appl
Sequence 589809,
Sequence 1203218,
Sequence 589808,
Sequence 1203217,
Sequence 31, Appl
Sequence 31, Appl
Sequence 121, Appl
Sequence 404, App
Sequence 74, App
Sequence 95, Appl
Sequence 55048, A
Sequence 120484,
Sequence 420484,
Sequence 485470,
Sequence 1098879,
Sequence 9980, Ap
Sequence 756577,
Sequence 756577, A
Sequence 14453, A
Sequence 14453, A

699 3 US-09-815-242-4505
699 3 US-09-815-242-8471
699 8 US-10-282-122A-7879
821 6 US-10-106-698-1828
914 3 US-09-983-802-123
914 3 US-09-984-490-123
914 3 US-09-973-278-36
986 12 US-10-301-480-589809
986 12 US-10-301-480-1203218
987 12 US-10-301-480-589808
987 12 US-10-301-480-1203217
1044 7 US-10-174-209-31
1044 10 US-10-972-587-31
1244 12 US-10-986-405-121
1244 2 US-08-781-986A-404
6254 8 US-10-329-624-404
9262 10 US-10-765-700-74
9277 6 US-10-084-817-95
245 8 US-10-424-599-55048
569 4 US-09-925-065A-420484
569 5 US-09-925-065A-420484
569 12 US-10-301-480-485470
569 12 US-10-301-480-1098879
201 15 US-11-124-368A-9980
465 4 US-09-925-065A-756577
465 5 US-09-925-065A-756577
742 4 US-09-925-065A-14453
742 5 US-09-925-065A-14453

; GENERAL INFORMATION:
 ; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
 ; APPLICANT: Huletsky, Ann
 ; APPLICANT: Rossbach, Valery
 ; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANCE
 ; FILE REFERENCE: TV/12287.92
 ; CURRENT APPLICATION NUMBER: US/10/479,674
 ; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: CA 2,348,042
 ; PRIOR FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 233
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 82
 ; LENGTH: 1957
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-10-479-674-82

Query Match 100.0%; Score 39; DB 9; Length 1957;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
 DB 905 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 867

RESULT 3
 US-09-452-599-169/c
 ; Sequence 169, Application US/09452599
 ; Patent No. US2002005101A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bergeron, Michel G.
 ; APPLICANT: Ouellette, Marc
 ; APPLICANT: Roy, Paul H.
 ; TITLE OF INVENTION: Specific and Universal Probes and Amplification Primers
 ; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
 ; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
 ; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
 ; FILE REFERENCE: 12287.31
 ; CURRENT APPLICATION NUMBER: US/09/452,599
 ; CURRENT FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 08/526,840
 ; PRIOR FILING DATE: 1995-09-11
 ; PRIOR APPLICATION NUMBER: 08/304,732
 ; PRIOR FILING DATE: 1994-09-12
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: Patent in ver. 2.1
 ; SEQ ID NO 169
 ; LENGTH: 2007
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-09-452-599-169
 Query Match 100.0%; Score 39; DB 3; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
 DB 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 4
 US-10-121-120-169/c
 ; Sequence 169, Application US/10121120
 ; Publication No. US20030180733A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bergeron, Michel G.
 ; APPLICANT: Ouellette, Marc
 ; APPLICANT: Roy, Paul H.
 ; TITLE OF INVENTION: Specific and Universal Probes and Amplification
 ; TITLE OF INVENTION: Primers

; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
 ; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
 ; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
 ; FILE REFERENCE: 12287.31
 ; CURRENT APPLICATION NUMBER: US/10/121,120
 ; CURRENT FILING DATE: 2002-04-11
 ; PRIOR APPLICATION NUMBER: 09/452,599
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 08/304,732
 ; PRIOR FILING DATE: 1994-09-12
 ; NUMBER OF SEQ ID NOS: 177
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 169
 ; LENGTH: 2007
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-10-121-120-169

Query Match 100.0%; Score 39; DB 7; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
 DB 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 5
 US-10-479-674-78/c
 ; Sequence 78, Application US/10479674
 ; Publication No. US20050019893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
 ; APPLICANT: Huletsky, Ann
 ; APPLICANT: Rossbach, Valery
 ; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS
 ; FILE REFERENCE: TV/12287.92
 ; CURRENT APPLICATION NUMBER: US/10/479,674
 ; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: CA 2,348,042
 ; PRIOR FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 233
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 78
 ; LENGTH: 2007
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 US-10-479-674-78

Query Match 100.0%; Score 39; DB 9; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
 DB 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 6
 US-10-479-674-90/c
 ; Sequence 90, Application US/10479674
 ; Publication No. US20050019893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Infectio Diagnostic (I.D.I.) Inc.
 ; APPLICANT: Huletsky, Ann
 ; APPLICANT: Rossbach, Valery
 ; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESIS
 ; FILE REFERENCE: TV/12287.92
 ; CURRENT APPLICATION NUMBER: US/10/479,674
 ; CURRENT FILING DATE: 2003-12-02
 ; PRIOR APPLICATION NUMBER: CA 2,348,042
 ; PRIOR FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 233

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-90

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
Db 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 7
US-10-479-674-91/c
; Sequence 91, Application US/10479674
; Publication No. US20050019893A1
; GENERAL INFORMATION:
; APPLICANT: Infectio Diagnostico (I.D.I.) Inc.
; APPLICANT: Huletsky, Ann
; APPLICANT: Huletsky, Valery
; TITLE OF INVENTION: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT
; FILE REFERENCE: TV/12287.92
; CURRENT APPLICATION NUMBER: US/10/479,674
; CURRENT FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: CA 2,348,042
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 233
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 91
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-479-674-91

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
Db 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 8
US-10-121-120-169/c
; Sequence 169, Application US/10121120
; Publication No. US20050042606A9
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Michel G.
; APPLICANT: Ouellette, Marc
; APPLICANT: Roy, Paul H.
; TITLE OF INVENTION: Specific and Universal Probes and Amplification
; TITLE OF INVENTION: Primers
; TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial
; TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clinical
; TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro
; FILE REFERENCE: 12287.31
; CURRENT APPLICATION NUMBER: US/10/121,120
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/452,599
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 08/304,732
; PRIOR FILING DATE: 1994-09-12
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
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US-10-121-120-169

Query Match      100.0%; Score 39; DB 9; Length 2007;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
Db 955 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 917

RESULT 9
US-10-724-972A-3141/c
; Sequence 3141, Application US/10724972A
; Publication No. US20040147734A1
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 3141
; LENGTH: 2028
; TYPE: DNA
; ORGANISM: S.epidermidis
US-10-724-972A-3141

Query Match      100.0%; Score 39; DB 8; Length 2028;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 39
Db 976 TTTTCTTTTCTCTATTAAATGATGTCGCGATTGTATTGC 938

RESULT 10
US-10-302-172-517
; Sequence 517, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803.1CNCp
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 517
; LENGTH: 3034
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (729)..(917)
US-10-302-172-517

Query Match      64.6%; Score 25.2; DB 8; Length 3034;
Best Local Similarity 78.9%; Pred. No. 3.2e+02;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGATTG 38
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2585 TATTTTTTTTTTGTATATATGCTGTGTGATTGATTG 2622

RESULT 11
US-09-925-065A-827806/c
; Sequence 827806, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827806
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827806

Query Match      63.1%; Score 24.6; DB 4; Length 644;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGATTG 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 TCTTCTTTTACTCTTAATGATGATGCCGATTGTTTC 149

RESULT 12
US-09-925-065A-827807/c
; Sequence 827807, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827807
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827807/c

Query Match      63.1%; Score 24.6; DB 5; Length 644;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGATTG 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 TCTTCTTTTACTCTTAATGATGATGCCGATTGTTTC 149

RESULT 13
US-09-925-065A-827806/c
; Sequence 827806, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827806
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827806

Query Match      63.1%; Score 24.6; DB 5; Length 644;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGATTG 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 TCTTCTTTTACTCTTAATGATGATGCCGATTGTTTC 149

RESULT 14
US-09-925-065A-827807/c
; Sequence 827807, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827807
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827807/c

Query Match      63.1%; Score 24.6; DB 5; Length 644;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTAATGATGATGCGGATTGATTG 39
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 TCTTCTTTTACTCTTAATGATGATGCCGATTGTTTC 149
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; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 827807
; LENGTH: 644
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-827807

Query Match 63.1%; Score 24.6; DB 5; Length 644;
Best Local Similarity 76.9%; Pred. No. 3.9e+02;
Matches 30; Conservative 0; Mismatches 9; Indels 0; Gaps 0; /
QY 1 TTTTCTTTTCTCTATTAATGATGCGGATGCTATTGC 39
DB 187 TCTTCTCTTTTACTCTTAATGATGCGCGGATGCTTTTC 149

RESULT 15

US-10-674-124A-21698/c
; Sequence 21698, Application US/10674124A
; Publication No. US2004019797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 21698
; LENGTH: 343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: D15S657
; FEATURE:
; OTHER INFORMATION: Located on chromosome 15
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 93129900
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 125770
US-10-674-124A-21698

Query Match 62.1%; Score 24.2; DB 9; Length 343;
Best Local Similarity 78.4%; Pred. No. 4.7e+02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TTTTCTTTTCTCTATTAATGATGCGGATGCTATT 37
DB 91 TATTCCTTTTCTATATATATATATGCGGAAGTGTT 55

Search completed: May 31, 2006, 23:02:26
Job time : 1014.2 secs

Db 48 CTTTCTCTGTTTGTATGACAATTG 76

RESULT 7
US-10-953-349-14981
; Sequence 14981, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14981
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-14981

Query Match 53.8%; Score 21; DB 6; Length 653;
Best Local Similarity 73.0%; Pred. No. 44;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TTTCTTTTCTCTATAATGATGCGCATGTATT 37
||||| ||||| ||||| ||||| |||||
Db 532 TTTCTTTTCTCTATAATGATGCGCATGTATT 568

RESULT 8
US-09-949-925-56/c
; Sequence 56, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: PZ023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 1478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-56

Query Match 53.8%; Score 21; DB 1; Length 1478;
Best Local Similarity 73.0%; Pred. No. 48;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TTTCTTTTCTCTATAATGATGCGCATGTATT 37
||||| ||||| ||||| ||||| |||||
Db 1471 TTTTCTTTTCTCTATAATGATGCGCATGTATT 1435

RESULT 9
US-10-953-349-22788/c
; Sequence 22788, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22788
; LENGTH: 1769
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-22788

Query Match 53.8%; Score 21; DB 6; Length 1769;
Best Local Similarity 73.0%; Pred. No. 49;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 TTTCTTTTCTCTATAATGATGCGCATGTATTG 38
||||| ||||| ||||| ||||| |||||
Db 471 TGTCTATTACTCTATTATTGAGTTTGTATTGTTG 435

RESULT 10
US-10-953-349-13689/c
; Sequence 13689, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13689
; LENGTH: 1789
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1782)..(1782)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1786)..(1786)
; OTHER INFORMATION: n is a, c, g, or t
US-10-953-349-13689

Query Match 53.8%; Score 21; DB 6; Length 1789;
Best Local Similarity 73.0%; Pred. No. 49;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 TTTCTTTTCTCTATAATGATGCGCATGTATTG 38
||||| ||||| ||||| ||||| |||||
Db 618 TGTCTATTACTCTATTATTGAGTTTGTATTGTTG 582

RESULT 11
US-10-953-349-3907
; Sequence 3907, Application US/10953349
; Publication No. US20060107345A1

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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3907
; LENGTH: 1795
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3907

Query Match          52.8%; Score 20.6; DB 6; Length 1795;
Best Local Similarity 74.3%; Pred. No. 66;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 TTTCTTTTCTCTAATGATGTCGCGATTGTAT 36
   ||||| ||||| ||||| ||||| ||||| |||||
Db 1602 TATCTATCTATATATATATATATCGGATTGTAT 1636

RESULT 12
US-10-953-349-24115
; Sequence 24115, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24115
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-24115

Query Match          52.3%; Score 20.4; DB 6; Length 728;
Best Local Similarity 71.1%; Pred. No. 68;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTAATGATGTCGCGATTGTATG 38
   ||||| ||||| ||||| ||||| ||||| |||||
Db 687 TTCCCTTTTGTATTAATGATGTCGGGAATTGATG 724

RESULT 13
US-10-953-349-11528
; Sequence 11528, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11528
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11528

Query Match          52.3%; Score 20.4; DB 6; Length 1451;
Best Local Similarity 71.1%; Pred. No. 74;
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```

Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTAATGATGTCGCGATTGTATG 38
   ||||| ||||| ||||| ||||| ||||| |||||
Db 1333 TTTTCTTTGCTTGTGTGTGTGTGTGATTTACTG 1370

RESULT 14
US-10-953-349-19450
; Sequence 19450, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19450
; LENGTH: 2150
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-19450

Query Match          52.3%; Score 20.4; DB 6; Length 2150;
Best Local Similarity 71.1%; Pred. No. 78;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TTTCTTTTCTCTAATGATGTCGCGATTGTATG 38
   ||||| ||||| ||||| ||||| ||||| |||||
Db 113 TTTCTTTGCTGTTCATCGTGTGTGTGTGTG 150

RESULT 15
US-11-217-529-5468/c
; Sequence 5468, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5468
; LENGTH: 2835
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5468

Query Match          52.3%; Score 20.4; DB 7; Length 2835;
Best Local Similarity 71.1%; Pred. No. 80;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 TTTCTTTTCTCTAATGATGTCGCGATTGTATGC 39
   ||||| ||||| ||||| ||||| ||||| |||||
Db 244 TCTCTTTTCTATACTAATATCAGGGCTTTTGGATAGC 207

Search completed: May 31, 2006, 21:22:06
Job time : 15.9259 secs
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